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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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protein search, using sw model . protein Š

April 25, 2006, 06:05:16; Search time 133.491 Seconds (Without alignments) 82.286 Million cell updates/sec Run on:

US-10-764-428-1 120 Title: Perfect

1 QVQLVQSGAEVKKPGASVKVSCKAS 25 score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2443163 seqs, 439378781 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

A_Geneseq_21:* .: geneseqp1980s:* Database:

geneseqp2000s:*geneseqp2001s:* geneseqp2003as:*geneseqp2003bs:* geneseqp2004s:*geneseqp2005s:* geneseqp1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20	Description	Adg90697 Anti-VEGF	Adu07258 IL-9 anti	Adt88325 Human IL-	Adu80305 Heavy cha	Ady31444 Human ant	Ady31447 Human ant	Ady31453 Human ant	Ady31459 Human ant	Ady31468 Human ant	Aar27045 Human hea	Aaw79211 Framework	Aae19676 Human gro	_	Adw87138 Anti-huma	Adx01239 Humanized	Adx27022 Human gro	Ady31315 Human ant	Ady31321 Human ant	Ady31327 Human ant	Ady31312 Human ant	Ady31336 Human ant	Ady59169 Anti-Tag-	Aeb13671 Human ant	Ahr61972 Monoclona
COLUMN TO STATE OF THE STATE OF	QI	ADQ90697	ADU07258	ADT88325	ADU80305	ADY31444	ADY31447	ADY31453	ADY31459	ADY31468	AAR27045	AAW79211	AAE19676	AAU70462	ADW87138	ADX01239	ADX27022	ADY31315	ADY31321	ADY31327	ADY31312	ADY31336	ADY59169	AEB13671	ARR61972
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	gth	25	25	25	25	25	25	25	25	25	30	30	30	30	30	30	30	30	30	30	30	30	30	30	32
*	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100
	Score	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120
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Abr57347 MatDC16 V Abo55410 Human gen	~	_			Abj18731 VH antibo			_		Aar92991 Homologou	~	Abg91863 Human ant			Adf09867 Anti-MUC1	Aar57475 Human HV3	Aar92078 Human HV3	Abg31425 Amino aci	Aay50952 Human ant
ABR57347 ABO55410	ABO59987	AEC20856	ADK18820	ABJ18728	ABJ18731	ABJ18730	ABJ18729	ABG75309	ABM79521	AAR92991	ABG78172	ABG91863	ADC99825	ADD05429	ADF09867	AAR57475	AAR92078	ABG31425	AAY50952
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120	120
25	27	28	29	30	31	35	9.6	3.6	. W	9.6	37	8	6	4 0	41	4.0	. 4	4	45

ALIGNMENTS

ADQ90697 standard; peptide; 25 AA.

ADQ90697;

(first entry) 21-OCT-2004 Anti-VEGF antibody heavy chain FR1 subgroup I peptide SEQ ID NO:1.

antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antinflammatory; antianglogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; angiogenic disorder; immunological disorder; anti-VEGF antibody; anti vascular endothelial cell growth factor antibody; heavy chain; FRI.

Homo sapiens Synthetic. WO2004065417-A2.

05-AUG-2004.

23-JAN-2004; 2004WO-US001844.

23-JAN-2003; 2003US-0442484P.

(GETH) GENENTECH INC.

Simmons L;

WPI; 2004-562149/54.

Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.

Claim 15; SEQ ID NO 1; 161pp; English.

The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid

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the amino acid found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervariable region. I wariable domain consensus sequence that has a hypervariable region. I (HVR1) and/or HVR2 amino acid sequence with the most sequence identity with a corresponding HVR1 and/or HVR2 sequence of the variable domain. Comprises the modified FR that has improved yield in cell culture compared to an antibody or antigen binding fragment. The antibody and antigen binding fragment bave cytostatic, antiinflammatory, antianglogenic and immunomodulatory activities, and can be used in antibody therapy. The methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in the particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and cumponic and immunological disorders. The present sequence represents a heavy chain FR1 peptide of an anti-VBGF (vascular cendothelial cell growth factor) antibody, which is used in the exemplification of the present invention.
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Sequence 25 AA;

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          Length 25;
                                0; Indels
          100.0%; Score 120; DB 8;
100.0%; Pred. No. 4.2e-10;
tive 0; Mismatches 0;
                                                       25
                                                                    1 QVQLVQSGAEVKKPGASVKVSCKAS 25
                                                         QVQLVQSGAEVKKPGASVKVSCKAS
Query Match
Best Local Similarity 100...
Conservative
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Gaps

RESULT 2 ADU07258

ADU07258 standard; peptide; 25 AA. (first entry) 13-JAN-2005 ADU07258;

Respiratory infection; human; interleukin-9 antagonist; IL-9; respiratory syncytial virus; anti-RSV antigen antibody; leukotriene modifier; asthma-like symptom; wheezing; allergy; immunomodulatory; anti-inflammatory; anti-viral; antibiotic; antifungal; mast cell modulator; virucide; antibacterial; fungicide; antiasthmatic; antiallergic; IL-9 antibody; variable heavy chain; VH; framework region. IL-9 antibody variable heavy chain (VH) framework region 1 sequence #1.

Homo sapiens

WO2004091519-A2.

28-OCT-2004.

12-APR-2004; 2004WO-US011329

11-APR-2003; 2003US-0462307P. 10-JUN-2003; 2003US-0477801P.

(MEDI-) MEDIMMUNE INC

Reed JL;

WPI; 2004-775524/76.

Managing, treating or ameliorating in a human subject a respiratory infection or its symptoms caused by bacteria, fungi or respiratory syncytial virus by administering an IL-9 antagonist.

Disclosure; SEQ ID NO 33; 276pp; English.

The invention relates to a method of managing, treating or ameliorating a respiratory infection or its symptom in a human subject by administering

an interlemental of the unbject an anti-respiratory syncytial virus (anticompanies antibody. The anti-RSV antigen antibody is palivizumab. The
method futcher comprises administering a leukotriene modifier, which is
method of preventing the development, onset or progression of asthma or
one or more asthma-like symptoms in a child, a method of preventing,
one or more asthma-like symptoms in a child, a method of preventing,
or control of preventing wheezing in a pre-term infant,
or child, a method of preventing, managing, treating or ameliorating asthma or an alleray or its symptoms in a human
cor more asthma-like symptoms or an alleray or its symptoms in a human
cor more asthma-like symptoms or an alleray or its symptoms in a human
cor more asthma-like symptoms in a child having or previously having a
core or more asthma-like symptoms in a child having or previously having a
core or more asthma-like symptoms in a child having or previously having a
core or more asthma-like symptoms in a child having or previously having a
core or more asthma-like symptoms in a child having or previously having a
core or more asthma-like symptoms in a child having or previously having a
core or more asthma-like symptoms in a human subject comprises administering or ameliorating
core preventing, managing, treating or ameliorating wheezing in a human subject comprises administering
core and instration of an IL-9 antagonist. Preventing, managing, treating
core an anti-immunoglobulin E (IGE) antibody, an anti-IL-4 antibody or a mast
core administering an IL-9 antagonist and at least one other antibody or a mast
core or an alleray or its symptoms in a human subject comprises
coll protease inhibitor. Preventing, managing, treating or ameliorating
anthma or an alleray or its symptoms in a human subject comprises
coll protease inhibitor. Preventing, managing, treating or ameliorating
content or a mast cell modifier, and antibodity or an antibodity or an antibody ö 100.0%; Score 120; DB 8; Length 25; 100.0%; Pred. No. 4.2e-10; Sequence 25 AA; against IL-9. Query Match

Gaps ö Indels 0; Mismatches 25; Conservative Best Local Similarity Matches 25; Conserv

1 QVQLVQSGAEVKKPGASVKVSCKAS 25 QVQLVQSGAEVKKPGASVKVSCKAS 25 ð 셤

ADT88325

ADT88325 standard; peptide; 25 ADT88325;

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Human IL-19 antibody VH framework region 1 seqid 33.

(first entry)

13-JAN-2005

respiratory; antiinflammatory; immunosuppressive; antiasthmatic; antiallergic; antianthritic; neuroprotective; antirheumatic; immunotoxin; angiogenesis inhibitor; TWR alpha antagonist; IL-9 antagonist; IL-9.
IL-9 antibody; 4D4; 4D4 H2-1 ID1; 4D4com-XF9; 4D4com-2F9; 7F3; 7IA10; 22D3; 7F3com-2H2; 7F3com-3H5; 7F3com-3D4; IL-9 associated disorder; respiratory infection; respiratory syncytial virus; parainfluenza virus; human metapneumovirus; inflammatory disorder; asthma; allergy; arthritis; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tramework region 1; variable heavy chain.

Homo sapiens

WO2004091510-A2

28-OCT-2004

12-APR-2004; 2004WO-US011172.

ä Ondek

Reed JL;

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The invention describes a new composition comprising a CD20 binding molecule having a binding affinity (Kd) for human CD20 of 5.0 x 10 -10 M or less, and a dissociation rate (koff) for human CD20 of 5.0 x 10 -4 s-1 or less. Also described is a method of treating B cell lymphoma. The CD20 binding molecules are useful for preparing a composition for treating B cell lymphoma. This is the amino acid sequence of human heavy chain framework region VHI DP7/21-2 FRL1 used in the creation of a CD20 binding
                                                                                                                                                                            New composition comprising a CD20 binding molecule having a binding affinity (Kd) for human CD20 and a dissociation rate (koff) for human, useful for preparing a composition for treating B cell lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA library; humanized antibody; antibody engineering; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human antibody heavy chain framework peptide - SEQ ID 276.
                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 120; DB 8;
100.0%; Pred. No. 4.2e-10;
tive 0; Mismatches 0;
                                                                                                             Davies J, Marquis DM, Allan BW,
                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 95; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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                                                                                (MOLE-) APPLIED MOLECULAR EVOLUTION
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13-OCT-2003; 2003US-0510741P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2004; 2004US-00923068
             20-MAY-2004; 2004WO-US015786.
                                      20-MAY-2003; 2003US-0471958P
                                                       52US-00471958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-180802/19.
                                                                                                                                         WPI; 2004-834173/82
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tes 25; Conserv
                                                                                                                                                        N-PSDB; ADU80309
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 AA;
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                                                       20-MAY-2004;
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                                                                                                             Watkins JD,
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                                                                                                                                                                                                                                     ö
                                                                                                                                         New IL-9 antibody comprising a variable heavy or light domain or a complementarity determining region having an amino acid sequence of e.g., 4D4, useful in treating or preventing e.g., respiratory infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy; antibody production; hematological disease; neoplasm; b-cell lymphoma; framework region; FRL1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 120; DB 8; Length 25; Local Similarity 100.0%; Pred. No. 4.2e-10; les 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody variable heavy chain framework region 1
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                                                                                                                                                                                                                    Disclosure; SEQ ID NO 33; 291pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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                11-APR-2003; 2003US-0462259P.
10-JUN-2003; 2003US-0477797P.
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                                                                                                                                                                                         inflammatory disorder.
                                                           (MEDI-) MEDIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; gene immune disorder;
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Sequence 25 AA;

Query Match

Best Loc Matches

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Indels

Length 25;

New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.

Disclosure; SEQ ID NO 276; 179pp; English.

WO2004103404-A1

02-DEC-2004

Homo sapiens.

24-FBB-2005

ADU80305;

RESULT 4 ADU80305

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ADY31453 standard; peptide; 25 AA.
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                       RESULT 7
                                            ADY31453
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                  The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework
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13-OCT-2003; 2003US-0510741P.
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Best Local Similarity
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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                        DNA library; humanized antibody; antibody engineering; heavy chain.
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                                          Human antibody heavy chain framework peptide - SEQ ID 285.
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13-OCT-2003; 2003US-0510741P.
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(first entry)
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                                                                                                                                          Homo sapiens
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The human framework sequence FR1 was used in the prodn. of humanised monoclonal antibodies comprising antigen binding sites (CDRs) of non human origen based on consensus sequence of CDRs. The sequence is a heavy chain framework region. The humanised antibodies or their chimeric variants may be used as therapeutic or diagnostic agents in order to combat e.g. glioma, melanoma or carcinoma. See also AAR27299-300 and AAR27037-51. (Updated on 25-MAR-2003 to correct PN field.)
light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monoclonal antibody; complementarity determining region; CDR; antigens;
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                                                                                                                                        Score 120; DB 9;
Pred. No. 4.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour; melanoma; carcinoma; glioma
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/label= Thr, Ser
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(first entry)
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                                                                                                            Sequence 25 AA;
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01-MAR-1993
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                                                                                                                                                                                                 New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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100.0%; Pred. No. 4.2
ive 0; Mismatches
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13-OCT-2003; 2003US-0510741P.
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                                              22-AUG-2003; 2003US-0497213P.
13-OCT-2003; 2003US-0510741P.
            20-AUG-2004; 2004US-00923068
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                                                                                                 (MEDI-) MEDIMMUNE INC
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                                                                                                                                 H, Dall-Acqua W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-180802/19.
                                                                                                                                                                    WPI; 2005-180802/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 AA;
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the invention relates to an antibody molecule having specificity for human tumour necrosis factor-alpha (TNFalpha) comprising a heavy or light confaint. The antibody or the compound comprising the antibody is useful for treating or manufacturing a medicament for treating a pathology mediated treating or manufacturing a medicament for treating a pathology mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha mediated confiseases which can be treated by the antibody include sepais, congestive confiseases which can be treated by the antibody include sepais, orgastive confiseases syndrome, acquired immunodeficiency syndrome (AIDS), allergies, distress syndrome, acquired immunodeficiency syndrome (AIDS), allergies, consensis, inflammatory bone disorders, blood coagulation disorders, burns, rejection episodes following organ or tissue transplant, Crohn's disease and autoimmune diseases, such as thyroiditis. The antibodies may also be used to reduce the side effects associated with TNFalpha generation during neoplasty therapy, to eliminate or reduce shock-related symptoms associated with the treatment or prevention of corpus for treating multiprocramation by use of an anti-lymphocyte antibody, for treating multiprocramation by use of an anti-lymphocyte antibody, for treating multiprocramation by use of an anti-lymphocyte antibody, for treating multiprocramation by use of an anti-lymphocyte antibody, for treating multiprocramation procramation of the invention cyrup consensus peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibody specific for human tumor necrosis factor (TNF)-alpha, useful for treating TNF-alpha-mediated diseases, e.g. congestive heart failure, septic or endotoxic shock, cachexia, adult respiratory distress syndrome.
                Human; tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR; complementarity determining region; rheumatoid; osteo-arthritis; sepsis; congestive heart failure; shock; tissue transplant; tuberculosis; AIDS; Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome; cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis; inflammatory bone disorder; Crohn's disease; autoimmune disease; burn; neoplasty therapy; immunomodulator; vulnerary; graft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weir ANC, Popplewell AG, Chapman AP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-2000; 2000GB-00013810.
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Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                  WO200194585-A1
                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002
                                                                                                                                                                                                                                                                                                                                     13-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Athwal DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU70462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       King DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU70462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This represents the amino acid sequence of the framework 1 region of human antibody clone Amu 5-3. This is used to consruct a humanised antibody LO-CD2a. The invention relates to the use of the monoclonal antibody (WAD) LO-CD2a or a humanised or a chimeric version of the LO-CD2a antibody for the inhibition of a T-cell mediated immune response in a patient. The MAD LO-CD2a (produced by Mybridoma cell line ATCC HB 1423) can bind to an epitope on the CD2 antigen of the human lymphocytes. The T-cell mediated immune response in a patient can be thin bitted by administering the WAD LO-CD2a or an antibody that binds the same human lymphocyte epitope as LO-CD2a. The method is used for preventing transplant rejection or for treating graft-versus-host disease
                                                                                                                                                                                                                                                                                                       Monoclonal antibody; MAb; LO-CD2a; humanised antibody; CD2 antigen; human lymphocyte; immune response; chimeric; graft-versus-host disease; T-cell; transplant rejection; autoimmune disease; Amu 5-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibition of T-cell mediated immune response with anti-CD2 monoclonal antibody LO-CD2a - used for preventing transplant rejection or for treating graft-versus-host disease or auto-immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                         Framework 1 region of human antibody clone Amu 5-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Col 35-36; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or for treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLVQSGAEVKKPGASVKVSCKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human group 1 consensus peptide #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE19676 standard; peptide; 30 AA
                                                                                                   AAW79211 standard; protein; 30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYLO-) UNIV CATHOLIQUE LOUVAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00027008.
93US-00119032.
95US-00407009.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Latinne D, Bazin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-556337/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                         21-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1993;
29-MAR-1995;
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                                                                                                                                                      AAW79211;
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Gaps

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AAE19676
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The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polymucleotides encoding different immunoglobulin binding protein (1980) polypeptides that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfered cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP array in plant cells. At least one peptide sequence has at least 75% sequence identity to a framework region (RR) of a native IgM, IgG, IgA, 196, IgB, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (CHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              light chain variable region; complementarity determining region; asthma; atopic dermatitis; allergic rhinitis; fibrosis; inflammatory bowel disease; Hodgkins disease.
                                                                                                                                                                                                                                                                                                                                                                                                      Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynuclectides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array.
complementarity determining region; framework region; IgBP;
transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
IgD; IgB; IgY; IgM; kappa; lambda; CHBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody engineering; antiasthmatic; dermatological; antiallergic; antinfiammatory; gastrointestinal-gen.; cytostatic; immunostimulant; diagnosis; interleukin-13; heavy chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 100.0%; Score 120; DB 5; Length 30; Local Similarity 100.0%; Pred. No. 5e-10; les 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-human interleukin-13 antibody-associated protein #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OVQLVQSGABVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1B; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADW87138 standard; protein; 30
                                                                                                                                                                                                                                                     02-MAY-2000; 2000US-00563222.
                                                                                                                                                                                                            02-MAY-2001; 2001WO-US014349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                           (BPIC-) EPICYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-055482/07
                                                                                                                                                                                                                                                                                                                                      Hatt AC, Hein MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 AA;
                                                                                                                             WO200183806-A1.
                                                                                         Homo sapiens
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                                                                                                                                                                      38-NOV-2001.
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Matches
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ID ADW6

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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated specific binding molecule (I) for human interleukin (IL)-13, comprising an antibody antigen-binding domain site composed of human antibody VH and VL domain comprising a set of complementarity determining regions (CDR's) HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3, (I) is useful for in vitro binding of (I) to human IL-13 or its fragment, and further involves determining the amount of binding of (I) to IL-13 or its fragment. (I) is useful in the manufacture of a medicament for treatment of a disease or disorder chosen from asthma, atopic dermatitis, allergic rhinitis, fibrosis, inflammatory bowel disease and Hodgkin's lymphoma. (I) is useful in diagnosing diseases such as asthma, atopic dermatitis, in the subject. (I) preferably neutralizes human IL-13. This sequence corresponds to protein used in the invention.
                                                                                                                                                                                                                                                                                   Novel isolated specific binding molecule for human interleukin-13, having antibody antigen-binding domain site composed of human variable heavy and light chain domains with complementarity determining regions, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody engineering; antibody production; immunosuppressive; immunotherapy; heavy chain variable region; light chain variable region; graft rejection; graft versus host disease; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 120; DB 9; Length 30; 100.0%; Pred. No. 5e-10; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                        Shorrock CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanized antibody generation peptide #10.
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 27; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGABVKKPGASVKVSCKAS 25
                                                                                                                                                                                         (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY
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                                                                                                                                                                                                                         Minter RR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00472281.
97WO-US012645.
                                                                                                                       31-MAR-2004; 2004GB-0007315.
31-MAR-2004; 2004US-0558216P.
24-MAY-2004; 2004US-0573791P.
                                                                          15-JUL-2004; 2004GB-00015857
                                                                                                            2003US-0487512P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.9
Matches 25; Conservative
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                                                                                                                                                                                                                             Jermutus L,
                                                                                                                                                                                                                                                          WPI; 2005-104209/12.
                                                                                                                                                                                                                                                                                                                                           treating asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30 AA;
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18-JUL-1997;
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                                                                                                            LS-JUL-2003;
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               GB2403952-A
                                             19-JAN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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The invention relates to a humanized antibody comprising the CDRs from LO-CD2a, produced by the cell line deposited as American Type Culture Collection (ATCC) HB11423, the humanized antibody containing in the framework of the heavy chain variable region of the humanized antibody, amino acids 47,67,70,72,76,85, and 87, and one, two, three, or four of amino acids 12, 13, 28, and 48 of the rat LO-CD2a heavy chain variable region of 118 amino acids, fully defined in the specification. The antibody is useful for preventing or inhibiting graft rejection, graft versus host disease or autoimmune disease. This sequence corresponds to a peptide used in the invention.
                                                                                                                                                                                            New humanized antibody comprising the complementary determining regions (CDRs) from LO-CD2a, useful for preventing or inhibiting graft rejection, graft versus host disease or autoimmune disease.
                                                                           Bazin H, Latinne D, Kaplan R, Kieber-Emmons T,
White-Scharf ME;
                                                                                                                                                                                                                                                                                        Example 7; SEQ ID NO 52; 126pp; English.
                (UYLO-) UNIV CATHOLIQUE LOUVAIN. (BIOT-) BIOTRANSPLANT INC.
                                                                                                                                                     WPI; 2005-129962/14.
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Postema CE;

Gaps ö Query Match 100.0%; Score 120; DB 9; Length 30; Best Local Similarity 100.0%; Pred. No. 5e-10; Matches 25; Conservative 0; Mismatches 0; Indels ò g

Sequence 30 AA;

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Search completed: April 25, 2006, 06:15:07 Job time : 136.491 secs

us-10-764-428-1.rpr

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Ig heavy chain V r Ig
                                                                            April 25, 2006, 06:15:41; Search time 21.2264 Seconds (without alignments) 113.322 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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seq length: 200000000
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chain	heavy chain V r	chain	chain	chain	chain	U	heavy chain pre								
Ig	Ig	Ig	Ig	βI	Ig	Ig									
831698	PH0959	G1HUBU	PH0961	PH0962	PH0958	S44108	PH0957	B33548	PH0955	PH0952	A33548	PH0954	S46394	C33548	B32274
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116	116	117	119	120	122	123	125	126	127	128	129	132	132	133	135
97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5	97.5
117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117
								38	_	_					

ALIGNMENTS

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RiTomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V. A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26910
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26920
C;Accession: S26920
M: M: M: M: Malter, G: Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
J. Mol. Biol. 227, 776-798, 1992
A;Atitle: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; WUID:93021117; PMID:1404388
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AjAolecule type: DNA
AjAolecules: 1-98 «TOMA
AjCross-references: UNIPARC:UPI00001163FB; EMBL:Z12309; NID:G32958; PIDN:CAA78179.1; PIC
Cj.Superfamily: immunoglobulin V region; immunoglobulin homology
Cj.Koywords: heterotetramer; immunoglobulin
Fi15-98/Domain: immunoglobulin homology <IMM>
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                               C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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100.0%; Score 120; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.9e-10;
vative 0; Mismatches 0;
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Ig heavy chain V region (DP-1) - human (fragment)
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Best Local Similarity 100.(
Matches 25; Conservative
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
                                                                                                  Accession: S26910
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A;Cross-references: UNIPARC:UPI000011644A; EMBL:Z14071; NID:g32969; PIDN:CAA78451.1; PID A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26913
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
J; Mol. Biol. 227, 776-798, 1992
A;Aritle: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
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C; Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession. S26919
C; Accession. S26919
R; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Wol. Biol. 227, 776-798, 1992
J; Wol. Biol. 227, 776-798, 1992
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V A; Reference number: S26885; WuID: 93021117; PMID: 1404388
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100.0%; Score 120; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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; Pred. No. 1.9e-10;
0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.9e-10; Matches 25; Conservative 0; Mismatches 0;
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Ig heavy chain V region (DP-12) - human (fragment)
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Ig heavy chain V region (DP-14) - human (fragment)
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hes 25; Conservative 0
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A; Residues: 1-98 <TOM>
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      1-98 <TOM>
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A;Status: preliminary
A;Nolecule type: DNA
A;Reaidus: 1-98 <TONA
A;Reaidus: 1-98 <TONA
A;Cross-references: UNIPARC:UPI000031F36; EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
A;Residues: 1-98 <TOM>
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin N region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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326938
19 heavy chain V region (DP-75) - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: S26938
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26938
A;Accession: S26938
A;Accession: Capiens (man)
A;Molecule type: DNA
                                                                                                                                                                     Ig heavy chain V region (DP-15) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 826918
R;Tomlinson, I.M.; Walter, G; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: 826885; MUID:93021117; PMID:1404388
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 826912
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: $26885; MUID:93021117; PMID:1404388
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1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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25; Conservative 0
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Length 116;

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Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 25; Conservative 0; Mismatches 0:
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A,Molecule type: mRNA
A,Residues: 20-116 <MAR>
A,Cross-references: UNIPARC:UPIO00017372B
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25;
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$31667
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 331667
R;Culsinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the;
A;Reference number: 331667
A;Reference number: 331667
A;Reference type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-116 <CUI>A;Cuss-references: UNIPARC:UPIO00011647F; EMBL:214215; NID:g37799; PIDN:CAA78584.1; PIL
C;Superfamily: immunoglobulin N region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;33-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region - human
C; Species: Homo sapiens (man)
C; Species: Jo. Peb-1995 #sequence_revision 20-Peb-1995 #text_change 23-Jul-1999
C; Accession: 821925
R; Priedman, D.F.
R; Priedman, D.F.
R; Priedman, D.F.
R; Priedman, D.F.
R; Priedman, S21925
A; Reference number: 821923
A; Reference number: 821923
A; Reference number: 821923
A; Status: preliminary
A; Reference DNA
A; Residues: 1-111 < PRI>A; Cross-references: UNIPARC: UPIO000115FA1; EMBL: X60503; NID:g33626; PIDN: CAA43023.1; PIC
C; Genetics:
A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                          Ig heavy chain V region (clone RPTS7H), rheumatoid factor - human (c.species: Homo sapiens (man) C.f.Species: Homo sapiens (man) C.f.Species: Homo sapiens (man) C.f.Species: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000 C.f.Accession: S69899 R.f.Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J. R.f. Tamen, I. I. Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J. A.f.tile: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune responsation: S69899 A.f.Ccession: S69899 A.f. A.f. Status: preliminary; translation not shown A.Status: preliminary; translation not shown A.Status: preliminary; translation not shown A.F. Residues: 1-104 KRAM>
                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UP1000011664D; EMBL:234893; NID:9509803; PIDN:CAA84376.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 120; DB 2; 100.0%; Pred. No. 2e-10;
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Matches 25; Conservative
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Matches 25; Conserv
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C;Accession: 800476; 834013
R;Matsuda, F.; Lee, K.H.; Nakai, S.; Sato, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Pukuha Rsmotsuda, F.; Lee, K.H.; Daylor Basto, T.; Kodaira, M.; Zong, S.Q.; Ohno, H.; Pukuha A;Title: Dispersed localization of D segments in the human immunoglobulin heavy-chain localization of A;Reference number: S00476; MUID:88296408; PMID:2841108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL:X07448; NID:g33104; PIDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: $00476
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPROT: P23083; UNIPARC: UPI00001179DB; EMBL: X07448; NID: g33104; PIDN
A; Morte: the authors translated the codon AGT for residue 89 as Met
B; Mariette, X.; Tsapis, A.; Brouet, J.C.
R; Mariette, X.; Tsapis, A.; Brouet, J.C.
A; Mariette, X.; Tsapis, Bequence analysis of the variable domains of four human monoclonal
A; Title: Nucleotidic sequence analysis of the Variable domains of four human monoclonal
A; Reference number: $34001; MUID: 93209281; PMID: 7681398
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                                                                                                                                                                                                                                                                                                                                             Ig heavy chain precursor V region (V35) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
        Gape
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C; Keywords: heterotetramer; immunoglobulin
F;1-19,Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (V35) #status predicted <WAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-117 <REC>
A; Cross-references: UNIPROT: P01743; UNIPARC: UPI000012CEE1
A; Note: the sequence was determined from the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 120; DB 1; 100.0%; Pred. No. 2.2e-10;
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A;Map position: 14q32.33-14q32.33
A;Introns: 16/1
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A; Map position: 14q32.33-14q32.33
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,Molecule type: DNA
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 318552
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, B.; HEMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: $18551; MUID:92037524; PMID:1935893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPARC:UPI0000115FEB; EMBL:X62107; NID:937833; PIDN:CAA44017.1; PIU
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Froduct: Ig heavy chain V-I region (HG3) #status predicted <WAT>
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                             Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-3) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                   Length 117;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
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A/Molecule type: DNA
A/Residues: 1-117 <SHI>
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Best Local Similarity 100.1
Matches 25; Conservative
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Best Local Similarity 100.'
Matches 25; Conservative
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Best Local Similarity 100.
Matches 25; Conservative
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S31680
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Ig heavy chain V region precursor (VI-3b) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: S1855; S26916
A;Ribin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; Hc EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: clt A;Recession: S18551; MUID:92037524; PMID:1935893
A;Recession: S18553
A;Accession: S18553
A;Accession: S18553
A;Accession: S18553
A;Accession: S18553
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
T. Mol. 257, 776-798, 1999
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V.
A;Reference number: S26885, MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 20-117 <TOM>
A;Cross-references: UNIPARC:UP10000116402; EMBL:Z12327; NID:g32871; PIDN:CAA78197.1; PID
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (VI-3b) #status predicted
F;34-117/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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Best Local Similarity 100.0%;
Matches 25; Conservative 0
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GenCore version 5.1.7
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sw model - protein search, using OM protein April 25, 2006, 06:05:44 , Search time 133.491 Seconds (without alignments) 132.131 Million cell updates/sec Run on:

1 QVQLVQSGAEVKKPGASVKVSCKAS 25 US-10-764-428-1 120 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters:

2166443 seqs, 705528306 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq_length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Tabase :

UniProt_05.80:*
.: uniprot_sprot:*
:: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1					SUMMAKIBS		
Regult No.	Score	Query	Query Match Length	08	ID	Description	
-	120	100.0	117	н	HV1B HUMAN	рошо	
~	120	100.0	117	ч	HV1G HUMAN	рошоц	
m	120	100.0		~	Q96QS0_HUMAN	homo	
4	120	100.0		~	Q6N091_HUMAN	рошо	
Ŋ	117	97.5		Н	HV1A HUMAN	P01742 homo sapien	
9	117	97.5		~	Q6NSA4 HUMAN	homo	
-	117	97.5	480	~	Q6PJF1_HUMAN	Q6pjf1 homo sapien	
- αο	117	97.5	498	7	Q6N041 HUMAN	homo	
6	116	ဖ	150	N	O9Y298 HUMAN	homo	
10	114	95.0	119	~	Q9UL94 HUMAN	homo	
11	114	95.0		~	Q9UL92 HUMAN	homo	
12	114	95.0		~	Q9UL95 HUMAN	homo	
13	114	95.0	244	~	Q652C8 HUMAN	homo	
14	113	94.2		7	O96QR9 HUMAN	homo	
15	112	93.3	4	7	Q6P089_HUMAN	homo	
16	112	93.3	519	N	QSEBM2_HUMAN	роц	
11	111	92.5		N	Q9GYZ2_MOUSE	m Bum	
18	110	91.7	125	N	Q6PIL0_HUMAN	omou.	
13	110	91.7	147	-	HV1C HUMAN	homo	
50	109	90.8		~	Q6N030 HUMAN	homo	
21	108	90.0		~	Q7Z7PS_HUMAN	homo	
22	107	89.2		Н	HV1D HUMAN	рошо	
23	107	89.2		Н	HV1B HUMAN	homo	
24	107	89.2		~	095978 HUMAN	095978 homo sapien	
25	105	87.5		~	Q569B1_RAT	Q569b1 rattus norv	
56	104	86.7		~	Q6N095 HUMAN	homo	
27	103	85.8		~1	HV1F HUMAN	_	
78	103	85.8		~	Q9D8L4 MOUSE	mus m	
	103	85.8	496	~	Q96DK0 HUMAN	homo	
30	103	85.8	S	7	Q6MZW0_HUMAN	homo	
31	102	85.0	484	(7	Q99LA6_MOUSE	Q99la6 mus musculu	

1 QVQLVQSGAEVKKPGASVKVSCKAS 25

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O8wy24 homo sapien Q4km15 mus musculu Q8vdc9 mus musculu Q6zp87 homo sapien Q5bk05 rattus norv Q6pjb2 mus musculu Q5fw11 mus musculu Q4qqw0 rattus norv Q8vcx7 mus musculu Q58e61 mus musculu Q9ul89 homo sapien Q9d9b8 mus musculu
2 Q8WY24_HUMAN 2 Q4KML5_MOUSE 2 Q6ZP87_HUMAN 2 Q5BKO5_MOUSE 2 Q6ZP87_HUMAN 2 Q5BKO5_RAT 2 Q6PU32_MOUSE 2 Q5FV33_RAT 2 Q9UWT1_MOUSE 2 Q5FV33_RAT 2 Q8VCX7_MOUSE 2 Q5BK31Z2_RAT 2 Q8UCX7_MOUSE 2 Q5BK61_MOUSE 2 Q5BK61_MOUSE 2 Q5BK61_MOUSE 2 Q5BK61_MOUSE 2 Q5DSBR61_MOUSE 3 Q9DSBR61_MOUSE
4 4 4 4 6 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
1002 1001 1001 1001 1001 1001 1000
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ALIGNMENTS

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                                POI743;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V-I region HG3 precursor.
Homo mappiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83144028; PubMed-6298778; R., Givol D.; Rechavi G., Ram D., Glazer L., Zakut R., Givol D.; "Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, J00240; AAA52988.1; -; Genomic_DNA.

RISSP: PO1751: 1NQB.

SKR; PD1743; 20-116.

GO; GO:0003576; C:extracellular region; NAS.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0005855; P:immune response; NAS.

InterPro; IRR003896; Ig.v.

SMAT; SMO0406; IGV; I.KB; I.

FROSITE; PSSOB3981; IG LIKE; I.

Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 120; DB 1;
100.0%; Pred. No. 1.2e-10;
tive 0; Mismatches 0;
117 AA.
PRT;
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   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
       HV1B HUMAN
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Gaps

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Putative matrix cell adhesion molecule-3.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGN091 HUMAN PRELIMINARY; PRT; 500 AA.
OGN091;
O6N091;
O5-UUL-2004 (TYEMBLrel. 27, Last sequence update)
O5-UUL-2004 (TYEMBLrel. 27, Last sequence update)
O5-UUL-2004 (TYEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686C02220 (Fragment).
Name-DKFZp686C02220;
Name-DKFZp686C02220;
Name-DKFZp686C02220;
Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Wambutt R., Heubner D., Mawes H.W., Weil B., Amid C., Osanger A., Probo G., Han M., Wiemann S.;
Probo G., Han M., Wiemann S.;
Probo G., Han M., Wiemann S.;
Robitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL; BX646625; CAE45779.1; -; mRNA.

R SMR; G00091; 270-478

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

R Pfan; SM00409; IG; 4.

R SMART; SM00409; IG; 4.

R SMART; SM00409; IG; 4.

R SMART; SM00406; IGV; 1.

R R PROSITE; PS50835; IG_LKE; 4.

R PROSITE; PS50835; IG_LKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 120; DB 2; Length 159; 1 Similarity 100.0%; Pred. No. 1.6e-10; 25; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match
Local Similarity 100.0%; Pred. No. 5.1e-10;
Nes 25; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                  Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                      EMBL; AY039025; AAK82649.1; -; mRNA.
HSSP; P01869; 1AE6.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig_v.
SMART; SM04406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain.
SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 AA; 54160 MW; 3C423A17D65A41B4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 OVOLVQSGAEVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLVQSGAEVKKPGASVKVSCKAS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Human rectum tumor;
The German Human cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appothetical protein
                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                Tilson M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EME outstation the Buropean Bioinformatics Institute. There are prestrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mariette X., Teapls A., Brouet J.C.; "Nucleotidic sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated
                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
MEDLINES #8926408; PubMed=2841108;
MATSUNG #8926408; PubMed=2841108;
MATSUNG F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
Ohno H., Fukuhara S., Honjo T.;
Ohno H., Fukuhara S., Honjo T.;
Inspersed localization of D segments in the human immunoglobulin
heavy-chain locus.";
EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Immunol. 23:846-851(1993).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE, PS50835, IG_LIKE, 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 117 Ig heavy chain V-I region 120 ×117 Ig-like. 117 117 AA, 13009 MW, BEGICEGIPBCE97BD CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X07448; -; NOT_ANNOTATED_CDS; Genomic_DNA.
PIR; S00476; HVHU35.
HSSP; PO1751; 1NOB.
SMR; P23083; 20-117.
Ensembl; ENSG00000130076; Homo sapiens.
                                                                                                                     01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Homo sapiens (Human)
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                                                                             117 AA
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                                                                                PRT;
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Q96QSO;
01-DEC-2001 (TEMBLEE) 19,
01-DEC-2003 (TEMBLEE) 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 25; Conservative
                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7681398;
                                                                           HV1G HUMAN
P23083;
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                           RESULT 2
HV1G HUMAN
HV1G HUMAN
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Gaps

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RESULT 3

ઠે 셤 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,

05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) IGHV1-69 protein.

Homo sapiens (Human)

NUCLEOTIDE SEQUENCE

NCBI_TaxID=9606;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,
Strausper R.D., Collins F.S., Wagner L., Sheafer C.F., Bhat N.K.,
Alberlul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Alberlul S.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Boufferd G.G.,
Antiting W., Madan A., Young A.C., Shevchenko Y., Boufferd G.G.,
Allakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
All Rederation and initial analysis of more than 15,000 full-length human

62

38 QVQLVQSGAEVKKPGASVKVSCKAS

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                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V-I region EU.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Blochemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gall W.B., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-71064024; PubMed-5489771;
Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
Waxdal M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.5%; Score 117; DB 1; 96.0%; Pred. No. 3.5e-10;
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SMR; P01742; 1-102.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_v.
                                                                                117 AA
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1; Mismatches
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                                                                           PRT;
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MEDLINE-71064027; PubMed=4923144;
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                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                HV1A_HUMAN
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RESULT 5
HV1A HUMAN
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Q6NSA4 HU
ID Q6NSI
AC Q6NSI
DT 05-J1
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC070333; AAH70333.1; -; mRNA. HSSP; P01751; 1A6W.

SMR; Q6NSA4; 21-116. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig_v.

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

mouse cDNA sequences."

and

NUCLEOTIDE SEQUENCE.

TISSUE=Pooled; NIH MGC Project;

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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                    SWART; SMO0406; IGV; 1."
PROSITE; PSSG835; IG LIKE; 1.
Immunoglobulin domain.
SEQUENCE 120 AA; 13035 MW; 64620PAC874585D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    20 QVQLVQSGAEVKKPGSSVKVSCKAS 44
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                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 96.0
nes 24; Conservative
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TISSUE=Lung;
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Length 117;

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HSSP; P01751; 1Abm.
SMR; Q6N041; 268-476.
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SEQUENCE
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The German Human cDNA Consortium;
Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX640710; CAE45829.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                       97.5%; Score 117; DB 2; Length 480; 96.0%; Pred. No. 1.5e-09; ive 1; Mismatches 0; Indels
                                                                                                                                                                                             Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016381; AAH16381.1; -; mRNA.
HSSP; P01061; IADQ.
                                                                                                                                                                                                                                                                                                              Hypothetical protein.
REOUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKF2p686016217 (Fragment).
Name-DKF2p686016217,
Homo sapiens (Human).
                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                               498 AA.
                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                                                                                                                                                                               20 QVQLVQSGAEVKKPGSSVKVSCKAS 44
                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                         InterPro; IPR003599; IG.
InterPro; IPR00310; Ig-like.
InterPro; IPR00310; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP07654; Cl-set; 3.
SMART; SM00407; IG21; 3.
SMART; SM00407; IGC1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                           QGN041_HUMAN PRELIMINARY;
QGN041;
                                                                                                                                                                                                                                                                                                                                                l Similarity 96.0
24; Conservative
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                                                                                                                                                                                      TISSUE=Lung;
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Ensembl; ENSG0000130076; Homo sapiens.
GO; GO:0015887; C:integral to plasma membrane; NAS.
GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
InterPro; IPR001596; Ig_v.
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Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VII inactivation: study with an
IgG4 monclonal antibody derived from a hemophilia A patient with
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96.7%; Score 116; DB 2; Length 150;
Best Local Similarity 96.0%; Pred. No. 6.5e-10;
Matches 24; Conservative 0; Mismatches 1; Indels
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ224083; CAAI1829.1; -; mRNA.
HSSP; P01857; 1HZH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 19 Potential.
150 150
150 AA; 16031 MW; 563D164AB22802D5 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 117; DB 2;
Pred. No. 1.5e-09;
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INTERPRETATION OF THE CONTROL OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OVOLVOSGAEVKKPGASVKVSCKAS 25
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PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
Q9Y298 HUMAN
ID Q9Y298 HUMAN PRELIMINARY;
AC Q9Y298;
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nes 24; Conservative
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Blood 92:496-506(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein-
NON TER 1
SEQUENCE 498 AA;
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20 QVQLVQSGAEVKXPGASVKVSCKVS 44

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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92.0%; Pred. No. 1.1e-09;
tive 2; Mismatches 0;
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EMBL; AR035022; AAD56258.1; -; mRNA.
HSSP; P01751; INQB.
Ensembl; RNSG00000130076; Homo sapiens.
InterPro; IPR07110; Ig-11ke.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGV; 1.
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HSSP; P01751; INOB.
HSSP; P01751; INOB.
HSSP; P01751; INOB.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
INTERFEC; IPR007110; Ig-like.
INTERFEC; IPR007110; Ig-like.
INTERFEC; IPR007110; Ig-like.
INTERFEC; IPR07110; Ig-like.
INTERFEC; IPR07110; Ig-like.
INTERFEC; IPR07110; Ig-like; I.
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                           119 AA.
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Q9UL92;
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Best Local Similarity 92.0'
                        QUL94_HUMAN PRELIMINARY;
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NCBI_TaxID=9606;
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Mammalia, Butheria, Buarchontoglires, Primates; Catarrhini, Hominidae;
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Local Similarity 92.0%; Score 114; DB 2; Length 125;
Local Similarity 92.0%; Pred. No. 1.1e-09;
Les 23; Conservative 2; Mismatches 0; Indels
                                                                                                                              Length 124;
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MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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125 AA; 13516 MW; 0D3CD5C232488RAC CRC64;
                                                         124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
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Last annotation update)
                                                                                                                              Query Match
Best Local Similarity 92.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 2; Mismatches 0
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HSSP, P01751; 1NQB.

EMBL, ENGO00000130076; Homo sapiens.

InterPro; IPR07110; Ig-like.

InterPro; IPR0715; Ig-like.

SMART; SM00406; IGV; 1.

PROSTIE; PS50835; IG_LIKE; 1.
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PROSITE; PS50835; IG_LIKE; 1.
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Q6SZC8;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UL95_HUMAN PRBLIMINARY;
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NUCLEOTIDE SEQUENCE.
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                                                      NON TER
SEQUENCE
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                               Query Match 95.0%; Score 114; DB 2; Length 244; Best Local Similarity 96.0%; Pred. No. 2.2e-09; Matches 24; Conservative 0; Mismatches 1; Indels
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Pred. No. 6.6e-10;
0; Mismatches 1; Indels
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EMBL, AX039026; AXR82650.1; -; mRNA.
HSSP; P01750; 1QNZ.
Ensembl; ENSG00000153613; Homo sapiens.
                                                                                                                                                                                                                                                                                   244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
Kontermann R.E., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
EMBL; VIONOT; CRA73500.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
SMART; SM00409; IG.; 2.
SMART; SM00409; IG.; 2.
PROSITE; PS50835; IG_LIKE; 2.
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SEQUENCE 52 AA; 5560 MW; 838755B1D18CB976 CRC64;
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CGF0089_
05-UTL-2004 (TYEMBLrel. 27, Created)
05-UTL-2004 (TYEMBLrel. 27, Last sequence update)
05-UTL-2004 (TYEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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Last annotation update)
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O96QR9;
O1-DEC-2001 (TrEMBLrel. 19, C.
O1-DEC-2001 (TrEMBLrel. 19, L.
O1-OCT-2003 (TrEMBLrel. 25, L.
Hypothetical protein.
Homo sapiens (Human).
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ilarity 96.0%;
Conservative
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0966R9 HUM
0966R8
AC 0966R8
DT 01-DE
DT 01-DE
DT 01-DE
DE HYPOTO
OC BUKAR
OC BUKAR
OC MAMMA
OC NCBI
RN (11)
RP TI180
RR TI180
RR HSSP;
DR HSSP;
DR HSSP;
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DR HSSP;
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066089 HUM
1D Q6608
AC Q6608
AC Q6608
DT 05-JU
DT 05-JU
DD HYDOT
OS HOMO
OC 
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       STTERNARARETES
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Blate N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Saress M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S.J., Malek J.M., Gay L.J., Hulyk S.W.,
N. Halton D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Mazny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: BCO65733, AAH65733.1; -; mRNA.
HSSP; P01751; 1A6W.
SNR; O6P089; 250-458.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003595; Ig-like.
InterPro; IPR003595; Ig-like.
InterPro; IPR003595; Ig-like.
InterPro; IPR003595; Ig-like.
InterPro; IPR003596; Ig-like.
InterPro; IPR003596; Ig-like.
InterPro; IPR0040595; Ig-like.
SMART; SM00409; IG-like; 4.
SWART; SM00406; IG-like; 4.
PROSITE; PS00290; IG-MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 480 AA; 51997 MW; ZE286C57E4F0ED65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB-Glandlar pool- thyroid;
Strausberg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                          April 25, 2006, 06:25:05; Search time 33.7264 Seconds (without alignments) 61.284 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, P
Sequence 4, P
Sequence 7, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16,
Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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Sequence
Sequence
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Sequence
Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                   Issued Patents AA:*

1: /cgn2 6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2 6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/H COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/PGTUS_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/RGTUS_COMB.pep:*
6: /cgn2 6/ptodata/1/iaa/RB_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-137-117D-157
US-08-137-117D-157
US-08-436-717-146
US-08-436-717-152
US-08-436-717-152
US-08-436-717-157
US-08-477-998-52
US-08-569-147-54
US-09-563-222C-133
US-09-563-22C-133
US-09-269-921-133
US-09-269-921-133
US-09-254-180C-150
US-09-254-180C-151
US-09-254-180C-151
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US-08-290-592E-16
PCT-US95-10053-13
PCT-US96-09448-16
                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKAS 25
                                                                                                                                                                      572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                Listing first 45 summaries
                                       OM protein - protein search, using sw model
                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                            Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                     US-10-764-428-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                      Database :
                                                                                                                        Sequence:
                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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Sequence 53, Appli Sequence 1, Appli Sequence 3, Appli Sequence 75, Appli Sequence 41, Appli Sequence 41, Appli Sequence 17, Appli Sequence 90, Appli Sequence 91, Appli Sequence 128, Appli Sequence 128, Appli Sequence 128, Appli Sequence 22, Appli
US-10-330-613A-53 US-09-899-866-1 US-08-899-866-3 US-08-899-866-5 US-08-89-896-5 US-08-861-521-41 PCT-US55-01219-41 US-08-545-809A-91 US-08-545-809A-91 US-08-545-809A-105 US-08-545-809A-105 US-08-545-809A-128 US-08-545-809A-128 US-09-490-153-22 US-09-490-153-22 US-09-490-153-22 US-09-490-153-22
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988011000000000000000000000000000000000
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120 120 120 120 120 120 120 120 120 120
24 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

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APPLICANT: TSUCHIYA, Masayuki
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: BALDANHA, JOSES, Steven
APPLICANT: SALDANHA, JOSES,
ITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENTO, Koh
APPLICANT: BENTOG, Wary
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHABED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFTATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Weakington STATE: D.C. COUNTRY: USA ZIP: 2007-5109 COMPUTER RRADABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53466/126/AAOK
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Patent No. 5795965
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WEGNER, Harold C. 258
REGISTRATION NUMBER: 25.258
REFERENCE/DOCKET NUMBER: 534
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-137-117D-146
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATENT NO. 5/301/97

GENERAL INCEMENTION:
APPLICANT: Bazin, Herv
APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
NUMBER OF SEQUENCES: 96
CORRESPONDENCE JE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Carella, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
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                                                                                                                                                      Query Match 100.0%; Score 120; DB 1; Length 30; Best Local Similarity 100.0%; Pred. No. 1.3e-10; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 120; DB 1; Length 30; 100.0%; Pred. No. 1.3e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 15 inch diskette
COMPUTER: 16 inch diskette
COMPUTER: 16 inch diskette
COMPUTER: 16 inch diskette
COMPUTER: 16 inch diskette
CLASSIFICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-193
APPLICATION NUMBER: 08/027,008
FILING DATE: 06-MAR-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 06-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: 01stein, Ellict M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-146
TELECOMMUNICATION INFORMATION:
TOTAL TELECOMMUNICATION INFORMATION:
TOTAL TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TOTAL TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TOTAL TELECOMMUNICATION INFORM
                                                                                                                                                                                                                                                                                                                                     QVQLVQSGAEVKKPGASVKVSCKAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-08-477-877B-52
Sequence 52, Application US/08477B77B
; Patent No. 5730979
                                                             OTHER INFORMATION: Ser."
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-08-137-117D-146
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                                                                       ;
US-07-946-421-11
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TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-137-117D-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TSUCHITA, Masayuki
APPLICANT: TSUCHITA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: JONES, Steven
APPLICANT: ALDANHA, Jose
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREE: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTY: USA
ZIP: 20007-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk.
                                                                                                               SIAIE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: E10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIPICATION NUMBER: WO PCT/JP92/00544
PILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-32084
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
PREDEDENTALION NUMBER: 25,258
PREDEDENTALION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                        ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGABVKKPGASVKVSCKAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 157, Application US/08137117D Patent No. 5795965 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INPORMATION FOR SEQ ID NO: 152:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acide
         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: ]
US-08-137-117D-152
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Sequence 52, Application US/08472281A

Sequence 52, Application US/08472281A

Sequence 52, Application US/08472281A

Sequence 52, Application

GRENEAL INFORMATION:

APPLICANT: Latinne, Herv

APPLICANT: Latinne, Dominique

TITLE OF INVENTION: LO-COZA Antibody and Uses Thereof for Inhibiting T-Cell Activa

NUMBER OF SEQUENCES: 96

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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SOFTWARE. PATOLIES. STOREM: V-LUOS, MOSTAMARE: PATOLIES. PATOLIES. PATOLIES. PATOLIES. PATOLIES. PATOLIES. PATOLIES. PATOLIES. PATOLIES. WOOR HILO. Version #1.30 CURRENT APPLICATION NUMBER: US/08/137,117D FILING DATE: 20-DEC-1993 CLASSITCATION. BATA: APPLICATION NUMBER: WO PCT/JP92/00544 FILING DATE: 24-APR-1992 PRICK APPLICATION NUMBER: WO PCT/JP92/00544 PRICK APPLICATION NUMBER: UP 4-32084 PRICK APPLICATION DATA: APPLICATION NUMBER: UP 3-95476 FILING DATE: 19-FEB-1992 PRICK APPLICATION NUMBER: UP 3-95476 FILING DATE: 25-APR-1991 ATTORNEY/AGENT INFORMATION: NUMBER: 25-258 REFERENCE/DOCKET NUMBER: 53466/126/AAOK TELECOMMUNICATION NUMBER: 53.258 REFERENCE/DOCKET NUMBER: 53.266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSER: Carella, Byrne, Bain, Gilfillan, ADDRESSER: Cacchi, Stewart & Olstein STREET: 6 Becker Farm Road CITY: Roseland STATE: New Jersey COUNTR: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 18M PS/2
OMPUTER: 18M PS/2
OMPUTER: 18M PS/2
OMPUTER: 18M PS/2
OMPRATE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,281A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION 1424
PRIOR APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
```

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; INFORMATION FOR SEQ ID NO: 1
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDENNES: single
; TOPOLOGY: linear
US-08-436-717-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-436-717-152
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US-08-436-717-152
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| Sequence 146, Application US/08436717
| Patent No. 5317708|
| APPLICANT: TSUCHIYA, Masayuki
| APPLICANT: TSUCHIYA, Masayuki
| APPLICANT: TSUCHIYA, Masayuki
| APPLICANT: BENDIG, Mary
| APPLICANT: BENDIG, Mary
| APPLICANT: BENDIG, Mary
| APPLICANT: JAMEN, Steven
| APPLICANT: JAMEN, Steven
| APPLICANT: ALLADANA, JOSE
| TITLE OF INVENTION: INTERLETKIN-6 RECEPTOR
| NUMBER OF SEQUENCES: 158
| CORRESPONDENCE ADDRESS:
| ADDRESSE: Poley & Lardner |
| STREET: 3000 K Street, N.W., Suite 500
| CITY: Washington | Street, N.W., Suite 500
| STATE: D.C. | COUNTRY: USA
| COMPUTER: IBW PC COMPATION |
| MEDIUM TYPE: PLOPPY disk |
| COMPUTER: IBW PC COMPATION |
| OPERATING SYSTEM: PC-DOS/MS-DOS |
| SOFTWARE: PREDABLE FORM: |
| MEDIUM TYPE: IBW PC COMPATION |
| OPERATING SYSTEM: US/08/436,717 |
| FILING DATE: 20-DEC-1993 |
| APPLICATION NUMBER: US/08/137,117 |
| FILING DATE: 24-APR-1992 |
| PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/137,117 |
| PLING DATE: 24-APR-1992 |
| PRIOR APPLICATION NUMBER: US/08/137,117 |
| PLING DATE: 25-APR-1991 |
| ATTORNEY ABENT |
| NAME: WECKET | 18 |
| NAME: WECKET |
| SALING DATE: 25-APR-1991 |
| NAME: WECKET |
| NAME: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0: Indela
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REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
   ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
RERERENCE/DOCKET NUMBER: 61750-142
TELEPONE: 201-994-1700
TELEPONE: 201-994-1744
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: allinear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQLVQSGAEVKKPGASVKVSCKAS 25
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TELEX: 90
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## SEQUENCE CHANCEREISTICS:

| SEQUENCE CHANCEREISTICS:
| TYPE: anino acida
| TYPE: anino acida
| STROUGH CHANCEREISTICS:
| Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
| Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
| OWINGSAEMINGTONERS OF OWNERS 0; Mismatches 0; Indels 0; Gaps 0;
| OWNERS OF OWNERS OF OWNERS 0; Mismatches 0; Indels 0; Gaps 0;
| OWNERS OF OWNERS OF OWNERS 0; Mismatches 0; Indels 0; Gaps 0;
| Matches 152, Application UB/08436717 |
| SEGUENCE 152, Application UB/08436717 |
| SEGUENCE 152, Application UB/08436717 |
| SEGUENCE 153, Application UB/08436717 |
| APPLICATION: OWNERS 154 |
| APPLICATION: OWNERS 154 |
| APPLICATION: OWNERS 154 |
| OWNERS 155 |
| OWNERS OF INVESTICS: INTERLECKIN'S RECEPTOR |
| MATCHES OF INVESTICS: INTERLECKIN'S RECEPTOR |
| MATCHES OF INVESTICS: INTERLECKIN'S RECEPTOR |
| OWNERS 155 |
| OWNERS 1
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STRANDEDNESS
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US-08-569-147-54
                                      JS-08-477-989B-52
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100.0%; Score 120; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
Query Match 100.0%; Score 120; DB 1; Length 30; Best Local Similarity 100.0%; Pred. No. 1.3e-10; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                Sequence 157, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHINA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: ARIDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INFERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PREDICT PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRILING DATE:
PRILOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNEY HAROLD C
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
TELLERAN: (202) 672-5300
TELLEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3000 K Street, N.W., Suite 500 CITY: Washington COLY: D.C.
                                                                                       1 QVQLVQSGABVKKPGASVKVSCKAS 25
                                                                                                                         1 OVQLVQSGABVKKPGASVKVSCKAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INPORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , TOPOLOGY: linear
US-08-436-717-157
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100.0%; Pred. No. 1.3e-10;
iive 0; Mismatches 0;
                                                                                                                 APPLICANT: Latinne, Dominique
APPLICANT: Kaplan, Ruth
APPLICANT: Kaber-Emmons, Thomas
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: White-Scharf, Mary
TITLE OF INVENTION: LO-CD2A Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEB: Carella, Byrne, Bain, Gilfillan,
ADDRESSEB: Cecchi, Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 54, Application US/08569147
; Patent No. 6180377
; GENERAL INPORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANISED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTINIT: U.S.A.

ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDErfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 03-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 03-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 03-SPP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Ellict M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-147
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESPOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKAS 25
Patent No. 5551983
CRNERAL INFORMATION:
APPLICANT: Bazin Vol.
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSES. 6 Becker Farm Road
CITY: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OVOLVOSGABVKKPGASVKVSCKAS 25

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1 QVQLVQSGAEVKKPGASVKVSCKAS
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                                                                         RESULT 13
US-09-830-748B-37
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Patent No. 6696620

GENERAL INPORMATION:
APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
TITLE OF INVENTION: IMMUNGIOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 068904-0501
CURRENT APPLICATION NUMBER: 108/09/563,22C
CURRENT PILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
SOUTHARE: PAPLICATION NUMBER: 09/563,222
NUMBER OF SEQ ID NOS: 182
SOUTHARE: PATENT VET. 2000-05-02
SOUTHARE: PATENT VET. 2000-05-02
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 133
LENGTH: 30
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                                                                                                                                                                          COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: Ploppy disk
COMPUTER: DATE: PLOPPY DATE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,147
FILING DATE: 25-March-1996
ATTORNEY/AGENT INPOMMATION:
NAME: TYLJIIO, DOCEON YARKO
REGISTRATION NUMBER: 35,719
RETERENCE/DOCKET NUMBER: 35,719
TELEPHONE: (215) 568-3100
TELEPAN: (215) 568-3100
TELEPAN: (215) 568-3109
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENDTH: 30 amino acids

"WAND: AMINO acids
"WAND: AMINO acids
"WAND: AMINO acids
"WAND: AMINO acids
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             CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Wo. 61803777is, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 120; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0;
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100.0%; Score 120; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0;
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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US-09-563-222C-133
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GENERAL INFORMATION:
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APPLICANT: Bazin, Herv,
APPLICANT: Latinne, Dominique
APPLICANT: Kaplan, Ruth
APPLICANT: Kaplan, Ruth
APPLICANT: Kaplan, Ruth
APPLICANT: Kaplan, Ruth
APPLICANT: Postema, Christina E.
APPLICANT: White-Scharf, Mary E.
APPLICANT: White-Scharf, Mary E.
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation
TITLE OF INVENTION: Proliferation
TITLE OF INVENTION: Proliferation
FILE REFERENCE: 61750-214
CURRENT APPLICATION NUMBER: US/09/462,140D
CURRENT FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 105
SEQ ID NO SEQ ID NOS: 105
LENGTH: 30
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Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 25; Conservative 0; Mismatches 0;
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Sequence 37, Application US/09830748B
Patent No. 6818749
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Patent No. 6849258
GENERAL INFORMATION:
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US-09-830-748B-37
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                                                                         RESULT 15
US-09-269-921-133
Sequence 133, Application US/09269921
Fatent No. 6699974
GENERAL INPORATION:
APPLICANT: Onc. Koichiro
APPLICANT: Onc. Koichiro
APPLICANT: Tauchiya, Masayuki
APPLICANT: Yoshimura, Yasushi
APPLICANT: Yoshimura, Yasushi
APPLICANT: Koishihara, Yasushi
APPLICANT: Soshimura, Yasushi
APPLICANT: Soshimura, Yasushi
APPLICANT: BRENERREN ESSHARED HUWAN ANTI-HM 1.24 ANTIBODY
FILE REPRENCE: 35029-20007 000
CURRENT APPLICATION NUMBER: US/09/269,921
CURRENT FILING DATE: 1990-04-01
SEALIER PILING DATE: 1990-03
RARLIER PILING DATE: 1990-03
RARLIER PILING DATE: 1996-10-03
MUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 133
LIVDR: DPT
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CORGANISM: Unknown
CORGANISM: Unknown
FEATURE:
COTHER INFORMATION: Description of Unknown Organism: HG3
PUBLICATION INFORMATION:
COURNAL: PROC. NATL. ACAD. SCI. USA
VOLUME: 80
VOLUME: 80
PAGES: 855-859
DATE: 1983
US-09-269-921-133
1 QVQLVQSGARVKKPGASVKVSCKAS 25
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Search completed: April 25, 2006, 06:28:39 Job time : 34.7264 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                       April 25, 2006, 06:58:17 ; Search time 108.962 Seconds (without alignments) 95.866 Million cell updates/sec
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(gn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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(gn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*);

(gn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*);
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 33621, A Sequence 214, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 130, Appl Sequence 47, Appl Sequence 47, Appl Sequence 17, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli	BINDING	Length 25; Indels 0; Gaps 0; USES THEREOF
US-10-029-386-33621 US-10-041-860-244 US-10-428-408A-21 US-10-428-894-21 US-10-699-874-21 US-10-699-874-21 US-10-837-904-130 US-10-032-0378-47 US-10-032-9888-47 US-10-029-9888-47 US-10-029-9888-47 US-10-029-9888-47 US-10-194-975-1 US-10-194-975-1 US-10-194-975-4 US-10-194-975-4 US-10-194-975-4 US-10-194-975-7 US-10-194-975-7 US-10-194-975-7	ALIGNMENTS 428 PRODUCING HUMANIZED NTIBODIES OR ANTIGEN 10/764,428 3 //442,484	ore 120; DB 5; dd. No. 1.8e-10; dismatches 0; AS 25 ANTIBODIES AND 97
N O O O O O O O O O O O O O O O O O O O	ASULT 1 Sequence 1, Application US/10764428 Publication No. US20040229310A1 GENERAL INFORMATION: APPLICANT: Simmons, Laura TITLE OF INVENTION: METHODS FOR PRITILE OF INVENTION: METHODS FOR PRITILE OF INVENTION: CULTURE FILE REPERENCE: 11669.120USU1 CURRENT APPLICATION NUMBER: US/10/CURRENT FILING DATE: 2004-01-23 PRIOR APPLICATION NUMBER: US 60/44 PRIOR FILING DATE: 2003-01-23 NUMBER OF SEQ ID NOS: 33 SOFTWARE: PATENTIN VERSION 3.1 SEQ ID NO 1 LENGTH: 25 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: FRI SGI	Query Match Best Local Similarity 100.0%; Pred Matches 25; Conservative 0; Mi Matches 1 QVQLVQSGAEVKKPGASVKVSCKAS DD 1 QVQLVQSGAEVKKPGASVKVSCKAS US-10-823-253-33 Sequence 33, Application US/10823253 Publication No. US20050002934A1 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: RECOMBINANT IL-9 FILE REFERENCE: 10271-112-999 FILE REFERENCE: 10271-112-999 FILE REFERENCE: 10271-112-999 FILE REPERENCE: 2004-04-12 CURRENT FILING DATE: 2003-04-11 PRIOR APPLICATION NUMBER: 60/462,259 PRIOR PLING DATE: 2003-04-11 PRIOR PLING DATE: 2003-04-11 PRIOR FILING DATE: 2003-04-11 PRIOR FILING DATE: 2003-04-13 SOFTWARE: PATENTING DATE: 2003-04-13 SOFTWARE: PATENTING DATE: 2003-04-13 SOFTWARE: PATENTING DATE: 2003-04-13 SOFTWARE: PATENTING DATE: 2003-04-13 SEQ ID NO 33
	4-428-1 ce 1, Application No. US2004 ation No. US2004 CANT: Simmons, IOF INVENTION: OF SEQ ID NOS: R	th Similarity 100 25 Conservative 100 25 Conservative 100 1 QVQLVQSGAEVKKPG 11 QVQLVQSGAEVKKPG 11 QVQLVQSGAEVKKPG 133-33 13. Application US 1070 11 UNUSKTION 10 ESCOMB 10 ENCOMB 10 ENCOM
120 120 120 120 120 120 120 120 120 120	RESULT 1 US-10-764-428-1 Sequence 1, Applicat. Publication No. US20, GENERAL INFORMATION: TITLE OF INVENTION: PILE REPERENCE: 116 CURRENT APPLICATION CURRENT FILING DATE PRIOR APPLICATION NO. USPION PRIOR APPLICATION NO. USPION FILING DATE: NUMBER OF SEQ ID NO. SOFTWARE: PATENTING SEQ ID NO. 1 LENGTH: 25 ITYPE: PRT TYPE: PRT CORGANISM: ARTIFICIAL CORGANISM: ARTIFICIAL FEATURE: CORGANISM: ARTIFICIAL CORGANISM: ARTIFICIAL CORGANISM: ARTIFICIAL CORGANISM: ARTIFICIAL CORGANISM: ARTIFICIAL COTHER INFORMATION: US-10-764-428-1	Query Match Best Local Sin Matches 25; 1 0 1 0 2 1 0 2 1 0 2 1 0 2 1 0 3 1 0 5 1 0
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US-10-923-068-285
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Best Local Similarity 100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.86-10;
Matches 25; Conservative 0; Mismatches
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Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: With Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: DameStroder, Melissa
ITILE REPERENCE: AE600US
FILE REPERENCE: AE600US
CURRENT APPLICANTION UNDERS: US/10/923, 068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FaetSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                        Sequence 95, Application US/10849615
Publication No. US20050025764A1
GENERAL INFORMATION:
APPLICANT: Allan, Barrett W.
APPLICANT: Davies, Julian
APPLICANT: Marquis, David M.
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: CD20 BINDING MOLECULES
FILE REFRENCE: AME-09916
CURRENT APPLICATION NUMBER: US/10/849,615
CURRENT APPLICATION NUMBER: US/10/849,615
CURRENT FILING DATE: 2004-05-20
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3:3
SEQ ID NO 95
LENGTH: 25
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; LOCATION: (1)...(25)
; OTHER INFORMATION: FRH1 VkI (DP7/21-2)
US-10-849-615-95
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ORGANISM: Homo sapiens
US-10-923-068-276
                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-823-253-33
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ORGANISM: Homo sapiens
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US-10-923-068-276
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100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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APPLICANT: Wu, Herren
APPLICANT: Wu, Herren
APPLICANT: Danschroder, Walliam
APPLICANT: Danschroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT PILING DATE: 2004-08-20
NUMBER: PSEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PAT
TYPE: PRT
TYPE: PRT
ORGANISM: Homo sapiens
US-10-923-068-279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 285, Application US/10923068
Publication No. US20050042664A1
GENERAL INFORMATION.
APPLICANT: WL, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Danschroder, Melissa
TITLE REFERENCE: AE600US
FILE REFERENCE: AE600US
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 285
LENGTH: 25
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Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
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Query Match
Best Local Similarity
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Publication No. US20050147607A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: REGEN GENOMER:

TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING RESPIRATORY CONDITIONS

FILE REFERENCE: 10271-113-999

CURRENT APPLICATION NUMBER: 40/462,307

PRIOR FILING DATE: 2003-04-11

PRIOR FILING DATE: 2003-04-10

PRIOR FILING DATE: 2003-6-10

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PATENTIN VESSION 3.2
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100.0%; Score 120; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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100.0%; Score 120; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 300, Application US/10923068

Publication No. US20050042664A1

GENERAL INFORMATION:
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: Damschroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
CURRENT PILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 300
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 291
LENGTH: 25
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ORGANISM: Homo sapiens
US-10-823-810-33
                                                                                                                               TYPE: PRT
COCCANISM: Homo sapiens
US-10-923-068-291
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US-10-923-068-300
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LENGTH: 25
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100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
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APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Brown, Derek Thomas
APPLICANT: Boplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TITLE OP INVENTION: Biological Products
TITLE OP INVENTION: Biological Products
FILE REPERENCE: Carp-0089
CURRENT APPLICATION NUMBER: 2001-06-06
PRIOR FILING DATE: 2001-06-06
                                                                                                                                                                               US-09-949-559-95
US-09-949-559-95
Sequence 95, Application US/09949559
Patent No. US20020151682A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Welr, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: Ring, David John
FILE REFERENCE: Carp-0095
CURRENT APPLICATION NUMBER: 001810.76B
PRIOR FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 130
SOFTWARRE: PatentIn version 3.1
SERGID NO 95
LENGTH: 30
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SOFTWARE: Patentin version 3.1
SEQ ID NO 95
LENGTH: 30
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Best Local Similarity
Matches 25; Conserv
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US-10-923-068-144
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Publication No. US20040199945A1

GENERAL INFORMATION:
APPLICANT: BICYTE PHARMACEUTICALS, INC.
APPLICANT: HIAT, ANDREW C.
APPLICANT: HIAT, ANDREW C.
TITLE OF INVENTION: IMMUNGCOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
TILE OF INVENTION: UMMUNGCOBULIN BINDING PROTEIN ARRAYS IN PLANT
CURRENT APPLICATION NUMBER: US/10/783,950

CURRENT APPLICATION NUMBER: US/09/563,222

PRIOR APPLICATION NUMBER: PCT/US01/14349

PRIOR FILING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 182

SEQ ID NO 133

LENGTH: 30
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US-09-563-222-142
; Sequence 142, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew;
; APPLICANT: Heatt, Andrew;
; TITLE OF INVENTION: EUKARYOTIC CELLS
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REPERENCE: 310098.406
; CURRENT PILING DATE: 2000-05-02
; WUMBER OF SEQ ID NOS: 197
; SEQ ID NO 142
; LENGTH: 30
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100.0%; Score 120; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
  0; Indels
0; Mismatches
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  25; Conservative
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; ORGANISM: Homo sapiens
US-10-783-950-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapien
US-09-563-222-142
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US-10-783-950-133
  Matches
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RESULT 14 US-10-728-420B-91

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APPLICANT: WOULER, SUSAN L.
APPLICANT: WOULER, SUSAN L.
APPLICANT: WOULER, SUSAN L.
APPLICANT: BURN, AIMEE
APPLICANT: BURN, AIMEE
TITLE OF INVENTION: RECROSIS FACTOR ALPHA IN COMBINATION WITH DISEASE MODIFYING
TITLE OF INVENTION: ANT: HERUMATIC DRUGS
TITLE OF INVENTION WIMBER: US/10/728,420B
CURRENT FILING DATE: 2003-12-05
PRIOR PILING DATE: 2003-12-05
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PASESEQ for Windows Version 4.0
LENGTHAR: 30
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US-10-728-420B-91
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100.0%; Score 120; DB 5;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 25; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 25; Conservative 0; Mismatches 0;
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Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Damschroder, Melissa
TITLE OP INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT PILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 144
LENGTH 30
TYPE: PRT
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Sequence 91, Application US/10728420B
Publication No. US20050042219A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-923-068-144
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April 25, 2006, 07:01:21 ; Search time 16.0377 Seconds (without alignments) 68.593 Million cell updates/sec
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1: /SIDS5/ptodata/1/pubpaa/US06_NEW_FUB.pep:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_FUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_FUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/US09_NEW_FUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_FUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US11_NEW_FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

US-11-105-268-33 US-11-108-135-4 US-11-108-135-4 US-11-108-135-4 US-11-226-886-48 US-11-226-886-48 US-11-226-886-48 US-11-226-886-88 US-11-226-325-200 US-11-226-325-200 US-11-054-669-1 US-11-054-669-2 US-11-054-669-3 US-11-054-669-3 US-11-054-669-1 US-11-054-669-1 US-11-054-669-1 US-11-054-669-1 US-11-054-669-1 US-11-054-669-1 US-11-054-669-1 US-11-054-669-1 US-11-064-554-16 US-11-064-554-16 US-11-064-554-18 US-11-064-554-18 US-11-064-5590-1 US-11-064-590-1 US-11-136-250-15 Sequence 1 US-11-136-250-15	Sequence 18, Appl
10 10 10 10 10 10 10 10 10 10 10 10 10 1	-136-250-18 Se
8	7 US-11
Match Length Match Length 100.0 30 100.0 30 100.0 30 100.0 30 100.0 30 100.0 98 100.	
Regult No. Score 1 120 2 120 3 120 4 120 7 120 110 120 111 120 114 120 115 120 116 120 117 120 118 120 119 120 21 120 22 120 23 120 24 120	25 120

Sequence 20, Appl Sequence 23, Appl Sequence 23, Appl Sequence 51, Appl Sequence 51, Appl Sequence 52, Appl Sequence 56, Appl Sequence 84, Appl Sequence 86, Appl Sequence 11, Appl Sequence 85, Appl Sequence 85, Appl	Sequence 86, Appl
9 7 US-11-136-250-20 9 7 US-11-084-554-23 9 7 US-11-136-250-23 9 7 US-11-155-843-51 9 7 US-11-155-843-52 9 7 US-11-155-843-53 9 7 US-11-155-843-63 9 7 US-11-155-843-84 9 7 US-11-155-843-85 9 7 US-11-155-843-85 9 7 US-11-175-648-11 1 US-11-177-648-13 1 US-11-177-648-13 1 US-11-177-648-13 1 US-11-177-648-13 1 US-11-177-648-13 1 US-11-177-648-13 1 US-11-177-648-13	3 7 US-11-177-648-86
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ALIGNMENTS

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US-11-105-269-33

US-11-105-269-33

US-11-105-269-33

Publication No. US2005052603041

Sequence 31, Application US/11105268

Publication No. US2005052603041

TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF

FILE REFERENCE: 1071-126-99

CURRENT PELINAN DAMPER: 2004-04-12

PRIOR PELICATION NUMBER: 60/561.845

PRIOR PELICATION NUMBER: 60/561.845

PRIOR PELICATION NUMBER: 60/561.845

PRIOR PELICATION NUMBER: 100.04; Score 120; DB 7; Length 25;

SEQ INNUMER: PRIOR NO. 100.04; Score 120; DB 7; Length 25;

GUBERY MATCH

US-11-105-268-33

QUBERY MATCH

DO NO. US20050560213A1

OVOLVOSGABVXKEGASVKVSCKAS 25

PABLICANT: Veri, MATLA CONCETTA

NAPLICANT: No. US2005050213A1

APPLICANT: No. US2005050213A1

APPLICANT: No. US2005050213A1

APPLICANT: Rankin, Christopher

TITLE OF INVENTION NUMBER: US 60/562, 804

PRIOR APPLICANTON NUMBER: US 60/562, 804

PRIOR APPLICANTON NUMBER: US 60/562, 804

PRIOR PLING DATE: 2004-04-15

PRIOR PLING DATE: 2004-04-16
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; OTHER INFORMATION: Framework sequence from human germline VH1-18 and JH6 - FR1
US-11-126-978-4
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Sequence 48, Application No. US20060057149A1

GENERAL INFORMATION:
GENERAL INFORMATION:
Hand, Liesie S.
APPLICANT: Johnson, Lesie S.
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST WEST NILE
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST WEST NILE
TITLE OF INVENTION: VIRUS AND THERAPEUTIC AND PROPHYLACTIC USES THEREOF
TITLE OF INVENTION: UNBER: US/11/226,886
CURRENT APPLICATION NUMBER: 05/609,766
PRIOR FILING DATE: 2004-09-13
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 48
LENGTH: 30
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Sequence 137, Application US/11226325

Bublication No. US20060008456A1

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, MASAYUKI

TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0274

CURRENT APPLICATION NUMBER: US/11/226,325

CURRENT FILING DATE: 2005-09-15

PRIOR APPLICATION NUMBER: US/09/509,098

PRIOR FILING DATE: 1998-10-02

PRIOR FILING DATE: 1998-10-02

PRIOR FILING DATE: 1998-10-03

PRIOR FILING DATE: 1998-10-03

PRIOR FILING DATE: 1998-10-03

NUMBER: OF SEQ ID NOS: 203

NUMBER: PATCH FULLY OF NOS: 203
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: 60/569,882
PRIOR FILING DATE: 2004-05-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 30
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ORGANISM: homo sapiens
PRATURE:
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
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| Sequence 111. Application No. US200600883A1
| GENERAL INFORMATION:
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Hammond, Phillip W.
| TITLE OF INVENTION: WITHOUS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
| TITLE OF INVENTION: WITHOUS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
| TITLE OF INVENTION: CONTEXT AND COMPOSITIONS THEREOF
| FILE REFERENCE: 185832/US/5
| CURRENT FILING DATE: 2004-12-03
| PRIOR PLILOGATION NUMBER: US 60/521,167
| PRIOR APPLICATION NUMBER: US 60/61,665
| PRIOR PILING DATE: 2004-06-13
| PRIOR PILING DATE: 2004-06-13
| PRIOR PLILING DATE: 2004-06-13
| PRIOR PLILOGATION NUMBER: US 60/619,483
| PRIOR PLINGATH: AND COMPANIES OF SECTION NUMBER: US 60/619,483
| PRIOR PLINGATH: AND COMPANIES OF SECTION NUMBER: US 60/619,483
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Publication No. US20060013810A1
GENERAL INFORMATION:
APPLICANT: Unango, Leslie Sydnor
APPLICANT: Huang, Ling
TITLE OF INVENTION: HUMANIZED FegammaRIIB-SPECIFIC ANTIBODIES AND METHODS OF USE THER
FILE REFERENCE: 11183-018-999
CURRENT FAPLICATION NUMBER: US/11/126,978
CURRENT FILING DATE: 2005-05-10
PRIOR APPLICATION NUMBER: 60/582,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Framework sequence from human germline VH1-18 and JH6 - FR1
US-11-108-135-4
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    PRIOR APPLICATION NUMBER: US 60/582,045
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/654,713
PRIOR FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 58
SOPTWARE: PartSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVQLVQSGAEVKKPGASVKVSCKAS 25
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                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-11-054-669-1
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; OTHER INFORMATION: Description of Artificial Sequence: Design of V
; OTHER INFORMATION: region of Natural Humanized Antibody (HG3)
US-11-226-325-200
                                                                                               FRATURE:
CHER INFORMATION: Description of Artificial Sequence: Amino acid
CHER INFORMATION: sequence of the H chain V region (1) HG3
CS-11-226-325-137
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100.0%; Score 120; DB 7; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/11054669
Publication No. US20050261480A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3
CURRENT FILING DATE: 2005-02-08
CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PATENT NOS: 124
SEQ ID NO 1
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATITY TSUCHIYA, MASAYUKI
TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0274
FULE REFERENCE: 053466/0274
CURRENT APPLICATION NUMBER: US/11/226,325
CURRENT FILING DATE: 2005-09-15
PRIOR APPLICATION NUMBER: PCT/JP98/04469
PRIOR PILING DATE: 1998-10-02
PRIOR FILING DATE: 1998-10-02
PRIOR FILING DATE: 1999-10-03
PRIOR PILING DATE: 1999-10-03
PRIOR PILING DATE: 1997-10-03
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 200
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ORGANISM: Artificial Sequence
                                                      TYPE: PRT
ORGANISM: Artificial Sequence
           SEQ ID NO 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 87
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Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
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Query Match 100.0%; Score 120; DB 7; Length 98; Best Local Similarity 100.0%; Pred. No. 3.7e-11; Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                          Sequence 2, Application US/11054669
; Sequence 2, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
   APPLICANT: Foote, Jefferson
; TILLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REPERRICE: 30219/US/3
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2002-07-12
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US,
FILE REPERENCE: 30219/US,
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SEQ ID NO 3
LENGTH: 98
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Best Local Similarity
Matches 25; Conserv
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Gaps

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Sequence 16, Application US/11084554

Publication No. US2005026079A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kellermann, Sirid-Ai

APPLICANT: Korver, Wouter

TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION

FILE REFERENCE: ABGENIX.100A

CURRENT PELING DATE: 2005-03-17

PRIOR APPLICATION NUMBER: 60/554,372

PRIOR APPLICATION NUMBER: 60/554,372

PRIOR APPLICATION NUMBER: 60/554,372

PRIOR APPLICATION NUMBER: 60/554,661

PRIOR APPLICATION NUMBER: 60/574,661

PRIOR APPLICATION NUMBER: 60/574,661

PRIOR APPLICATION NUMBER: 60/574,661

PRIOR ELING DATE: 2004-05-24

NUMBER OF SEQ ID NOS: 266

SOFTWARE: PASESEG FOR Windows Version 4.0

SEQ ID NO 16

LENGTH: 98
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| Publication No. US2005026679A1
| GENERAL INFORMATION:
| APPLICANT: Kellermann, Sirid-Ai
| APPLICANT: Kellermann, Sirid-Ai
| TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
| TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
| TITLE OF INVENTION: ANTIBODIES 1400GH V GENE MANIPULATION
| CURRENT APPLICATION NUMBER: US/11/084,554
| CURRENT FILING DATE: 2004-03-17
| PRIOR PILING DATE: 2004-03-19
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Best Local Similarity 100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0: Tndel.
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100.0%; Score 120; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/11/084,554
CURRENT FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR PILING DATE: 2004-03-19
PRIOR PILING DATE: 2004-03-19
PRIOR PILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 98
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Sequence 15, Application US/11084554

PUDICATION NO. US20050260679A1

GENERAL INFORMATION:
APPLICANT: Kellermann, Sirid-Ai
APPLICANT: Green, Larry L.
APPLICANT: Korver, Wouter
ITILE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
ITILE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Publication No. US20050261480A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3,
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT PILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR APPLICATION NUMBER: US 60/305,111
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PATENTIN PATENTIN VETSION 3.3
                                                                                                                                     APPLICANT: FOCACE, Jefferson
IIILE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 3013/9/03,3
FULRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR PILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.3
SEQ ID NO 4
LENGTH: 98
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                                                        ; Sequence 4, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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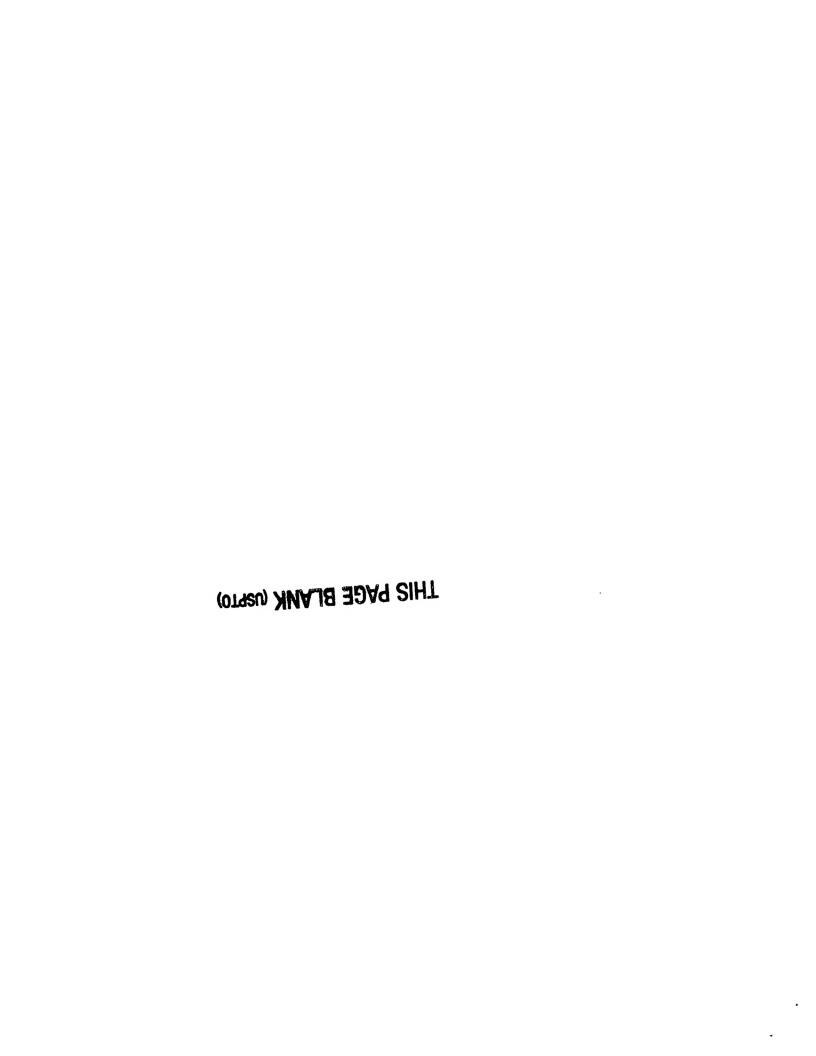
Gaps ö

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prior Application NUMBER: 60/574,661
prior Piling Date: 2004-05-24
i NUMBER OF SEQ ID NOS: 266
i SOFTWARE: FestSEQ for Windows Version 4.0
i SEQ ID NO 18
i LENGTH: 98
i TYPE: PRT
i ORGANISM: Homo sapiens
US-11-084-554-18
Query Match
Beet Local Similarity 100.0%; Pred. No. 3.7e-11;
Beet Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: April 25, 2006, 07:10:01 Job time : 16.2044 secs

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April 25, 2006, 06:05:16; Search time 133.491 Seconds (without alignments) 82.286 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A_Geneseq_21:* Database :

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

genesequ1980s:* genesequ2000s:* genesequ2000s:* genesequ2001s:* genesequ2003s:* genesequ2003as:* genesequ2004s:* genesequ2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No. is the score greater tha

	ų,	Anti-VEGF	Human ant	Human ant	Human ant	Human hea	Human ant	Human ant	Human ant	Anti-huma	Anti-MUC1	Anti-MUC1	Anti-huma	Anti-MUC1	Anti-MUC1	Human Fv	Human ant	Human ger	Human ger	Human ger	Germline	Anti-huma	Germline	Germline	Germline	
	Description	Adq90698		Abg98300	-	6	Ady31417	Aea21493		-	-			Add05453	Adf09891	Abg78215	Abg91906	Abo27105	Abo27103	Abo27106	Adc99848	Adc99817	Adc99844	Adc99836	Adc99816	
SUMMARIES	ΩI	AD090698	ADY31549	ABG98300	ABG98301	AAU70466	ADY31417	AEA21493	AEA21457	ADC99829	ADD05433	ADF09871	ADC99849	ADD05453	ADF09891	ABG78215	ABG91906	ABO27105	ABO27103	ABO27106	ADC99848	ADC99817	ADC99844	ADC99836	ADC99816	
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	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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ALIGNMENTS

RESULT 1

antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antinfilammatory; antiangiogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; angiogenic disorder; immunological disorder; anti-VEGF antibody; antibody; anti vascular endothèlial cell growth factor antibody; heavy chain; FRI. Anti-VEGF antibody heavy chain FR1 subgroup II peptide SEQ ID NO:2. ADQ90698 standard; peptide; 25 AA. (first entry) 21-0CT-2004 ADQ90698;

Homo sapiens. Synthetic.

WO2004065417-A2.

23-JAN-2004; 2004WO-US001844. 05-AUG-2004.

23-JAN-2003; 2003US-0442484P.

(GETH) GENENTECH INC.

Simmons L;

WPI; 2004-562149/54.

Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.

Claim 15; SEQ ID NO 2; 161pp; English

The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid

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the amino acid found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervariable region 1 (HYR1) and/or HYR2 amino acid sequence with the most sequence identity with a corresponding HYR1 sequence of the variable domain.

With a corresponding HYR1 and/or HYR2 sequence of the variable domain.

The antibody or antigen binding fragment variable domain comprises the condition improved yield in cell culture compared to an unmodified antibody or antigen-binding fragment. The antibody and antigen binding fragment have cytostatic, antiniflammatory, antiangiogenic and immunomodulatory activities, and can be used in antibody therapy. The methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in conducing antibodies or antigen binding fragment antibodies or antigen binding fragments in cell culture. The antibodies or antigen binding fragments and invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and cust of diagnose, treat, inhibit or prevent e.g. tumours and confirmantory, angiogenic and immunological disorders. The present sequence represents a heavy chain FRI peptide of an anti-VEGF (vascular cendothelial cell growth factor) antibody, which is used in the exemplification of the present invention.
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where the different amino acid is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA library; humanized antibody; antibody engineering; heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human antibody heavy chain framework peptide - SEQ ID 381.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 124; DB 8;
Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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position with a different amino acid,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu H, Dall-Acqua W, Damschroder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLQESGPGLVKPSQTLSLTCTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADY31549 standard, peptide, 25 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2004; 2004US-00923068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2003; 2003US-0497213P.
13-OCT-2003; 2003US-0510741P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-180802/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 AA;
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Best Local S
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The invention relates to an antibody which binds to an epitope on gp39, is new, where the epitope is distinct from the epitope bound by IDEC-131, and the antibody has a non-agonistic effect on T-cell activation and cinhibits gp39/CD40 interaction. Also included are: (1) an improved method treating a disease by modulating gp39 expression or inhibiting the gp39/CD40 interaction comprishing an antibody specific for gp39/CD40 interaction comprishing an antibody specific of T-cell activation; (2) an antibody which antagonises B-cell differentiation and antibody production, and is non-agonistic of T-cell activation; (3) a DNA sequence which encodes an antibody for of T-cell activation; (3) a DNA sequence which encodes an antibody defined above; (4) an expression vector, which contains a DNA sequence of (3); (5) a method of suppressing cortors and/or cellular immune responses against cells or vectors administering or after gene therapy comprising further administering prior, during or after gene therapy, an antibody defined above; and (6) cells, tissues or organs of the same or different species into a subject, where the improvement comprises administering an antibody defined above prior, during or after transplantation, to suppress immune egainst the transplanted cell, tissue or organ against the responses elicited by the transplanted cell, tissue or organ against the responses the antibody is useful for preventing graft rejection, and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies binding to an epitope on gp39, useful for preventing graft rejection, or for treating autoimmune diseases (e.g. diabetes, asthma or multiple sclerosis), and non-autoimmune diseases (e.g. graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody; variable region; light chain; heavy chain; VH; VL; gp39; CD40; T-cell activation; B-cell differentiation; framework region; cellular immune response; gene therapy; graft rejection; human; FR; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes; asthma; multiple sclerosis; allergy; diabetee mellitus; systemic lupus erythematosus; graft-versus-host disease.
                                                                              Gaps
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                                     Length 25;
                                                                              Indels
                                   100.0%; Score 124; DB 9;
100.0%; Pred. No. 5.8e-10;
ive 0; Mismatches 0;
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                                                                                                                                                QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                        1 QVQLQESGPGLVKPSQTLSLTCTVS
                                                                                                                                                                                                                                                                      ABG98300 standard; peptide; 30 AA.
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                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                        Local Similarity 100.
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Sequence 25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                       Query Match
                                                               Best Loc
Matches
                                                                                                                                                                                                                                                   ABG98300
ID ABGS
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for

peptide

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treating autoimmune diseases, e.g., rheumatoid arthritis, multiple sclerosis, diabetes, asthma, multiple sclerosis, allergic conditions, diabetes mellitus, or systemic lupus erythematosus, as well as non-autoimmune diseases such as graft-versus-host diseases (many other diseases and conditions are given in the specification). The antibodies are also useful in gene or cellular therapy, and to inhibit humoral and cellular immune responses against viral vectors. The present sequence is a framework region (FR) fragment of a human anti-gp39 antibody used to determine which amino acids should be humanised in a mouse anti-gp39
                  8888888888888
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Sequence 30 AA;

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Length 30;
                             Indels
100.0%; Score 124; DB 5;
100.0%; Pred. No. 6.9e-10;
ive 0; Mismatches 0;
                                                                               1 QVQLQBSGPGLVKPSQTLSLTCTVS 25
                                                             1 OVOLORSGPGLVKPSQTLSLTCTVS 25
Query Match 100.
Best Local Similarity 100.
Matches 25, Conservative
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Gaps

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ABG98301 standard; peptide; 30 AA. ABG98301

ABG98301;

08-JAN-2003 (first entry)

Human antibody 3d75d germline kappa chain variable region FR1.

Antibody; variable region; light chain; heavy chain; VH; VL; gp39; CD40; T-cell activation; B-cell differentiation; framework region; cellular immune response; gene therapy; graft rejection; human; FR; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes; asthms; multiple sclerosis; diabetes mellitus; systemic lupus erythematosus; graft-versus-host disease.

Homo sapiens.

WO200194586-A2.

13-DEC-2001.

06-JUN-2001; 2001WO-US018098

06-JUN-2000; 2000US-0209584P

(IDEC-) IDEC PHARM CORP.

New antibodies binding to an epitope on gp39, useful for preventing graft rejection, or for treating autoimmune diseases (e.g. diabetes, asthma or multiple sclerosis), and non-autoimmune diseases (e.g. graft-versus-host Anderson DR, Pan LZ, WPI; 2002-188261/24.

Kloetzer WS;

Rastetter WH,

Hanna N,

Disclosure; Page 47; 130pp; English.

disease).

The invention relates to an antibody which binds to an epitope on gp39, is new, where the epitope is distinct from the epitope bound by IDEC-131, and the antibody has a non-agonistic effect on T-cell activation and inhibits gp39/CD40 interaction. Also included are: (1) an improved method of treating a disease by modulating gp39 expression or inhibiting the gp39/CD40 interaction comprising administering an antibody specific for gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of T-cell activation; (2) an antibody which antagonises B-cell differentiation and antibody production, and is non-agonistic of T-cell activation; (3) a bNA sequence which encodes an antibody defined above; (4) an expression vector, which contains a DNA sequence of (3); (5) a method of suppressing

The invention relates to transforming a population of cells (e.g. plant cells), comprising using a library of two different polynucleotides encoding different immunoglobulin binding protein (1988) polypeptides

Disclosure, Fig 1B; 129pp; English.

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continued analogor certificat summurate responses escalarios continued analogor certificat summurate administering cell or gene therapy comprising further administering prior, during or after gene therapy, an antibody defined above; and (6) an improved method of treatment which involves the transplantation of cells, tissues or organs of the same or different species into a subject, where the improvement comprises administering an antibody defined above prior, during or after transplantation, to suppress immune casponses against the transplanted cell, tissue or organ, or to suppress immune creapings the transplanted cell, tissue or organ against the reponses elicited by the transplanted cell, tissue or organ against the creating autoimmune diseases, e.g., rhewmatoid arthritis, multiple contenting graft rejection, and for treating autoimmune diseases, e.g., rhewmatoid arthritis, multiple clarosis, allergic conditions, calcibates mellitus, or systemic lupus erythematosus, as well as noncutoimmune diseases such as graft-versus-host disease (many other calcibates mellitus as graft-versus-host disease (many other calcibate immune responses aginet viral vectors. The present sequence is a framework region (FR) fragment of a human anti-gp39 antibody used to determine which amino acids should be humanised in a mouse anti-gp39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynuclectides encoding binding protein polypeptides specific to ligand, selecting plant cells for preparing array.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
complementarity determining region; framework region; IgBP;
transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
numoral and/or cellular immune responses against cells or vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human heavy chain immunoglobulin framework region 1 #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 124; DB 5; 100.0%; Pred. No. 6.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IgD; IgE; IgY; IgM; kappa; lambda; CHBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                  molecule
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QVQLQESGPGLVKPSQTLSLTCTVS

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that specifically bind to a ligand or form one or more disulphide bonds with polypeptides in transfected cells, to generate an IgBP that binds to a ligand, and transformed plant cells are selected, and preparing an IgBP array in plant cells. At least one peptide sequence has at least 75% sequence identity to a framework region (FR) of a native IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is useful for preparing an immunoglobulin binding protein array, preferably heavy chain binding protein (CHBP) array in eukaryotic cells especially plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic cells (e.g. insect cells or mammalian cells). The CHBP is useful for discovery of e.g. screening assays of IgBPs having desired characteristics. The present sequence is a mammalian immunoglobulin derived peptide that may be incorporated into an IgBP of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA library; humanized antibody; antibody engineering; heavy chain.
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100.0%; Score 124; DB 9;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 25; Conservative 0; Mismatches 0;
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100.0%; Score 124; DB 5;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-180802/19
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This invention relates to a novel isolated human antibody that specifically binds to secretory leukocyte protease inhibitor (SLPI). The invention may be useful for the development of compounds with a cytostatic activity or for immunotherapy. The antibody, composition and methods are useful for treating and preventing cancer. The antibodies are useful for detecting the presence of SLPI in biological samples. The present sequence is that of a peptide which was used during the development of the novel antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human antibody that specifically binds to secretory leukocyte protease inhibitor (SLPI), useful for treating and preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhong H;
                                                                                                                                                                                                                                                                                                                                                                                                 Human anti-SLPI antibody-related peptide SegID57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human anti-SLPI antibody-related peptide SeqID21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallo ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody; cytostatic; immunotherapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody; cytostatic; immunotherapy; cancer
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                               1 QVQLQESGPGLVXPSQTLSLTCTVS
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                                                                                                                                                                                                               AEA21493 standard; peptide; 30 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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New human anti-MUC18 monoclonal antibodies, useful for treating a disease
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Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 25; Conservative 0; Mismatches n.
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                                                                                                                                                                                                                                                                                                       Larochelle WJ,
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                                                                                                                                    08-NOV-2004; 2004WO-US038634.
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                                                                                                                                                                                                                                                                                                          Chui D,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-367001/37
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                       WO2005047328-A2.
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                                                                               26-MAY-2005
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The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of WUC18 on the cell surface such as tumours, specifically melanoma, ossophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraspithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies The current sequence is that of the anti-human WUC18 antibody-related consensus protein of the invention derived from analysis of germline gene region proteins and anti-human WUC18 monoclonal antibody sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
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or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 124; DB 7;
100.0%; Pred. No. 2.2e-09;
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                                                                        Example 2; SEQ ID NO 58; 78pp; English.
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Best Local Similarity 100.
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel isolated human antibody that specifically binds to secretory leukocyte protease inhibitor (SLPI). The invention may be useful for the development of compounds with a cytostatic activity or for immunotherapy. The antibody, composition and enchods are useful for treating and preventing cancer. The antibodies are useful for detecting the presence of SLPI in biological samples. The present sequence is that of a peptide which was used during the development of the novel antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                        New isolated human antibody that specifically binds to secretory leukocyte protease inhibitor (SLPI), useful for treating and preventing
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cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody heavy chain, variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; consensus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-MUC18 monoclonal antibody-related consensus protein #9
                                                                                                                                                                                                                                                                                                                                           Length 95;
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                                                                                                                                                                                                          consensus protein of the invention.
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Best Local Similarity 100.
Matches 25; Conservative
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les 25; Conserv
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                                                                                                                                                                                                                                                                            Sequence 95 AA;
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                                                                                                                                                                                                                       anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                            Anti-human MUC18 antibody-related consensus protein SEQ ID 78.
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100.0%; Pred. No. 2.2e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; SEQ ID NO 78; 78pp; English.
QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD05453 standard; protein; 98 AA.
                                                                                              ADC99849 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2002; 2002WO-US041581.
                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-2001; 2001US-0346299P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0%;
                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-587113/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                        WO2003057838-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 98 AA;
                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                           lung cancer.
                                                                                                                                                            01-JAN-2004
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Gaps

28-DEC-2001; 2001US-0346414P. 26-DEC-2002; 2002WO-US041580

17-JUL-2003.

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The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises cumour growth in an animal. The tumour inhibition process comprises comprises comprises an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 animo acids given in the specification, and where the monoclonal antibody band inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the WUC18 antigen are useful for diagnosing and antibodies against the WUC18 antigen are useful for diagnosing and treating tumourse, inhibiting cell invasion associated with melanoma, or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-WUC18 antibody heavy chain, variable region,
             Anti-MUC18 antibody heavy chain variable region V4-31 consensus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                    monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccin
antigen; tumour metastasis; melanoma; metastatic; human; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 78; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLQESGPGLVKPSQTLSLTCTVS
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                                                                                                                                                                                                                                                                                           28-DEC-2001; 2001US-0346460P.
                                                                                                                                                                                                                                                 26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                                                                                                                                                         Gudas J, Bar-Eli M;
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                                                                                                                                                                                                                                                                                                                                  (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metastatic tumor
                                                                                                                                                                 WO2003057006-A2.
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      Length 98;
                                 Indels
/ Match 100.0%; Score 124; DB 7; Local Similarity 100.0%; Pred. No. 2.2e-09; nes 25; Conservative 0; Mismatches 0;
                                                             25
                                                                            QVQLQESGPGLVKPSQTLSLTCTVS 25
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Human Fv molecule hypervariable region related peptide #90.
                                                                                                                                                                                                                                                                                                                                        Szanton B,
                                                                                                                                                                                                                                                                                                                                        Guy R, Lipschitz O,
                                                                                                                                                                                                                                                                                                        (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                                                                                                                                                                                                                   29-DEC-2000; 2000US-00751181.
                                                                                                                                                                                                                            31-DEC-2001; 2001WO-US049440.
                                                                                                                                                                                                                                                                                                                                            Lazarovits J,
Peretz T;
                                                                                                                                                        WO200259264-A2
                                                                                                                    Homo sapiens
                                                                                                                                                                                         01-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                Plaksin D,
                                                                                                                                                                                                                                                                                                                                            Hagai Y,
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cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; consensus.

WO2003057837-A2.

Synthetic.

Anti-MUC18 monoclonal antibody-related consensus protein #19

(first entry)

12-PBB-2004

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ADF09891

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ADF09891 standard; protein; 98

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The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastaais. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence is a consensus sequence from an alignment between an MUC18 tumour antigen-specific monoclonal antibody of the invention and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, Fv molecule, hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.
                                                                                                                                                                            Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Levanon A;
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100.0%; Score 124; DB 7;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-619166/66.
                                                                                                                                                      WPI; 2003-598367/56
                                                                                                (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                   related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98 AA;
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                                                                                                                            Gudas J;
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Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favor of other cella.

Claim 13; Page 194-195; 232pp; English

The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with chanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scPv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, basecominoma, and melanoma, where the leukaemia cell is a coute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention

Sequence 99 AA;

Gaps ö Length 99; Query Match 100.0%; Score 124; DB 5; Length 9 Best Local Similarity 100.0%; Pred. No. 2.3e-09; Matches 25; Conservative 0; Mismatches 0; Indels

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Search completed: April 25, 2006, 06:15:10 Job time : 134.491 secs

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Sequence 20, Appl
Sequence 38, Appl
Sequence 36, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 45, Appl
Sequence 57, Appl
Sequence 67, Appl
Sequence 77, Appl
Sequence 17, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 5, Appli
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                                                                                                                                      April 25, 2006, 06:25:05; Search time 33.7264 Seconds (without alignments) 61.284 Million cell updates/sec
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*

1. /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-08-955-339-20
US-08-925-339-20
US-09-332-595-19
US-00-332-595-20
US-10-330-613A-58
US-10-10-194-975-36
US-10-194-975-36
US-10-330-613A-45
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US-10-330-613A-77
US-10-330-613A-77
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US-10-330-613A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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124
1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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Maximum Match 100%
Listing first 45 summaries
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28 124 100.0 119 2 US-09-467-903-5 Sequence 5, Appli 2 US-10-330-613A-25 Sequence 25, Appli 30 124 100.0 136 2 US-10-330-613A-25 Sequence 25, Appli 31 121 97.6 30 1 US-08-137-117D-128 Sequence 128, Appli 32 121 97.6 30 1 US-08-137-117D-128 Sequence 128, Appli 34 121 97.6 30 1 US-08-36-717-128 Sequence 128, Appli 35 121 97.6 30 1 US-08-354-840-21 Sequence 128, Appli 36 121 97.6 76 2 US-08-554-840-21 Sequence 21, Appli 36 121 97.6 76 2 US-08-925-339-21 Sequence 21, Appli 39 121 97.6 87 2 US-08-554-840-16 Sequence 16, Appli 42 121 97.6 97 2 US-10-330-613A-70 Sequence 16, Appli 42 121 97.6 96 2 US-10-330-613A-70 Sequence 62, Appli 43 121 97.6 97 2 US-10-330-613A-50 Sequence 62, Appli 44 121 97.6 97 2 US-10-194-975-51 Sequence 51, Appli 45 121 97.6 97 2 US-10-194-975-51 Sequence 51, Appli 45 121 97.6 97 2 US-10-194-975-51
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ALIGNMENTS

US-09-563-222C-137

j Sequence 137, Application US/09563222C

patent No. 6696620

GENERAL INFORMATION:
patent No. 6696620

GENERAL INFORMATION:
patent No. 6696620

j GENERAL INFORMATION:
patent No. 669904-0501

j TITLE OF INVESTION: IMMUNOCLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

rither Reference: 669904-0501

CURRENT PILING DATE: 2000-05-02

price Application NUMBER: 02/05-02

price Application NUMBER: 02/05-02

price Application NUMBER: 09/563,222

price Application NUMBER: 09/563,222

price Price Filing DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 182

SOOTWARKE: Patentin Ver. 2.1

SEQ ID NO 137

LENGTH: 30

TYPE: RR

CREANISM: Homo sapiens
US-09-563-222C-137

Query Match Best Local Similarity 100.0%; Pred. No. 2.3e-12; Length 30; Matches 25; Conservative 0; Mismatches 0; Indels 0;

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Gaps

8 8

RESULT 2
US-08-554-840-19
US-08-554-840-19
Sequence 19, Application US/08554840
SEQUENCE APPLICANT: BACK, Amelia
APPLICANT: BACK, Amelia
APPLICANT: NEWMAN, Roland A. TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
STATE: Virginia
STATE: Virginia

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RESULT 5
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USE UB-554-50
USE UB-554
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                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

TLING DATE: 07-NOV-1995

CLASSIPICATION NUMBER: US/08/554,840

FRIEDRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-127

TELECOMMUNICATION INFORMATION:

TELEPANDE: (703) 836-620

TELEPANCE: (703) 836-621

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 87 amino acids

TYPE: amino acids

TYPE: ADMINISTRESS: single
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United States
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MOLECULE TYPE: protein
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US-08-554-840-20
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US-608-25-39-19
US-608-25-39-19
US-608-25-39-19
Patent No. 6440418
Patent No. 6440418
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: BADLAN, Reduard A.
APPLICANT: NEWAYN, Reduard A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSES: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STRATE: Vidialia
COUNTRY: United States
COUNTRY: United States
COUNTRY: IBM PC COMPABLIS
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPABLIS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                Query Match 100.0%; Score 124; DB 2; Length 87; Best Local Similarity 100.0%; Pred. No. 7.7e-12; Matches 25; Conservative 0; Mismatches 0; Indels
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CLASSIFICATION:
PRIOR APPLICATION DATE:
PRIOR APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 012712-127
TELECOMMUNICATION NUMBER: 012712-127
TELEPHONE: (703) 836-6220
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
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LENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 87 amino acids
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                                                                                                    , MOLECULE TYPE: protein US-08-554-840-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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single
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MOLECULE TYPE: protein
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22313-1404
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US-09-332-595-20
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                                                                                     APPLICANT: BLACK, Amelia
APPLICANT: BLACK, Amelia
APPLICANT: BLACK, Amelia
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEGURNCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: BUTTHS, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STREET: United States
CONTENT: United States
CONTENT: United States
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BRACH PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/09332595
; Sequence 19, Application US/09332595
; Patent No. 6506383
; GENERAL INPORMATION:
    APPLICANT: BLACK, Amelia
    APPLICANT: BADLAN, Nabil
    APPLICANT: PADLAN, Nabil
    APPLICANT: PADLAN, Nabil
    APPLICANT: PADLAN, Nabil
    APPLICANT: PADLAN, COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
    TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
    NUMBER OF SEQUENCES: 28
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Burns, Doane, Swecker & Mathis
    STREET: P.O. Box 1404
    CITY: Alexandria
    STATE: Virginia
    STATE: Virginia
    STATE: United States
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100.0%; Pred. No. 7.7e-12;
tive 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
                          Sequence 20, Application US/08925339
Patent No. 6440418
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-332-595-19
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              US-08-925-339-20
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GENURAL INFORMATION:
| Pactent No. 6506383 | Pactent No. 6506383 |
| GENURAL INFORMATION: | APPLICANT: BLACK, Amelia | APPLICANT: BLACK, Amelia | APPLICANT: PADLAN, Roland A. | APPLICANT: NEWANN, Roland A. | APPLICANT: NEWANN, ROLAND A. | APPLICANT: NEWANN COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF INVERTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28 | CORRESPONDENCE ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: BUTHS, Doane, Swecker & Mathis | STREET: P.O. 1807 | P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BA PC COMPATIBLE
COMPUTER: BA PC COMPATIBLE
COMPUTER: BA PC COMPATIBLE
COMPUTER: BA PC COMPATIST
COMPARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,595
FILLING DATE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,595
FILING DATE:
CLIASIFFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/08/554,840
FILING DATE:
APPLICATION NUMBER: US/08/554,840
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REBERRENCE/DOCKET NUMBER: 012712-127
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-620
TELEFRAM: (703) 836-620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 124; DB 2; 100.0%; Pred. No. 7.7e-12;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                          1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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Best Local Similarity
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                                                                                                                                                                                                                                                                 Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 124; DB 2; Length 95; Best Local Similarity 100.0%; Pred. No. 8.5e-12; Matches 25; Conservative 0; Mismatches 0; Indels
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APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCIB ANTIGEN
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCIB ANTIGEN
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCIB ANTIGEN
TITLE OF INVENTION: ADGENIX. 022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT PILING DATE: 2001-12-26
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FRATEEQ for Windows Version 4.0
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCI8 ANTIGEN
FITLE REPERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 124; DB 2; Best Local Similarity 100.0%; Pred. No. 7.7e-12; Matches 25; Conservative 0; Mismatches 0;
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; Sequence 58, Application US/10330613A
; Patent No. 6924360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 78, Application US/10330613A Patent No. 6924360
TELECOMMUNICATION INFORMATION:
       ILENCHMENT (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 aming acids
                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                        TOPOLOGY: linear; MOLECULE TYPE: protein US-09-332-595-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-10-330-613A-58
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CRGANISM: Homo sapiens
US-10-330-613A-78
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LENGTH: 95
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US-10-194-975-36

Sequence 36, Application US/10194975

Patent No. 6881557

GENERAL INFORMATION:

APPLICATIVE FOOCE, Jefferson

TITLE OF INVENTION Super Humanized Antibodies

TITLE OF INVENTION Super Humanized Antibodies

CURRENT APPLICATION NUMBER: US/10/194,975

CURRENT PILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US 60/305,111

PRIOR APPLICATION NUMBER: US 60/305,111

NUMBER OF SEQ ID NOS: 122

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 36

LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FOOTE, Jefferson
TILLE OF INVENTION: Super Humanized Antibodies
TITLE OF INVENTION: Super Humanized Antibodies
FILE REPERSINCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR PILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
LENGTH: 99
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US-10-144-975-38
Sequence 38, Application US/10194975
Patent No. 6881557
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-36
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Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                       Length 99;
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| Sequence 46, Application US/10330613A
| Patent No. 6924360
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
| FILE REFERENCE: ADGENIX. 022A
| CURRENT APPLICATION NUMBER: US/10/330,613A
| CURRENT PILLING DATE: 2002-12-26
| PRIOR PILLING DATE: 2001-12-18
| NUMBER OF SEQ ID NOS: 90
| SOFTWARE: PERSENCE: AMINDOMS Version 4.0
| SEQ ID NO 46
| LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-330-613A-45
; Sequence 45, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; TITLE Gudas, Jan BERNIX.022A
; TITLE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT APPLICATION NUMBER: 60/346299
PRIOR PILING DATE: 2001-12-18
; WINDER OF SEQ ID NOS: 90
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 45

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Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 8.9e-12;
Matches 25; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOPTWARE: Patentin version 3.1
SEQ ID NO 39
LENGTH: 99
                                                                                                                                                                                                                                                                                   1 QVQLQBSGPGLVKPSQTLSLTCTVS 25
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CORGANISM: Homo sapiens
US-10-330-613A-45
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                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-10-194-975-39
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Qy 1 QVQLQBSGPGLVKPSQTLSLTCTVS 25

RESULT 15

RESULT 15

US-10-330-613A-57

Sequence 57, Application US/10330613A

Patent No. 6924360

Sequence 57, Application US/10330613A

Patent No. 6924360

SEQUENCE 57, AND SEQUENCE AGAINST THE MUCIB ANTIGEN

TITLE OF INVERTION: ANTIBODIES AGAINST THE MUCIB ANTIGEN

PILE REFERENCE: ABGENIX.022A

TITLE OF INVERTION ANTIBODIES AGAINST THE MUCIB ANTIGEN

PRIOR PAPLICATION NUMBER: 09/346299

PRIOR PILING DATE: 2001-12-18

SEQ ID NO 57

LENGTH: 99

TYPE: PRIOR FILING DATE: 2001-12-18

SEQ ID NO 57

CREATE FASTESQ for Windows Version 4.0

SEQ ID NO 57

LENGTH: 99

TYPE: PRI

ORGANISH: Homo sapiens

US-10-330-613A-57

Query Match

QY

1 QVQLQBSGPGLVKPSQTLSLTCTVS 25

DD

1 QVQLQBSGPGLVKPSQTLSLTCTVS 25

DD

1 QVQLQBSGPGLVKPSQTLSLTCTVS 25

DD

1 QVQLQBSGPGLVKPSQTLSLTCTVS 25

Search completed: April 25, 2006, 06:28:41
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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mode1 36 - protein search, using OM protein

Run on:

April 25, 2006, 06:15:41; Search time 21.2264 Seconds (without alignments) 113.322 Million cell updates/sec

US-10-764-428-2 124 1 QVQLQBSGPGLVKPSQTLSLTCTVS 25 score: Title: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

Database :

PIR 80:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Description	3 heavy	g heavy	heavy	g heavy c	g lambda chain	g heavy	heavy	g heavy	heavy	heavy	heavy		heavy	heavy	heavy	heavy	heavy	g heavy ch	н	pothetica	Ig heavy chain - h		heavy	Ig heavy chain V r					
:	QI.	S26801	S26803	830534	S31585	S26804	S26906	PH0876	S12421	S26807	S44125	S57464	B26340	S18557	S20780	A26340	844113	830530	831514	S31690	S31673	831676	831696	831586	137782	A24770	831512		S12416	826802
	80	7	~	~	0	~	~	~	~	~	0	N	7	~	~	~	~	7	7	~	~	~	7	~	7	~	7	~	~	0
	Length	66	66	130	137	97	97	97	86	66	105	115	116	116	118	118	121	123	128	130	130	137	139	139	140	140	155	155	97	66
	Match		100.0	100.0	100.0	97.6	97.6	97.6	97.6	97.6	97.6	97.6	-	•	97.6	97.6			97.6	97.6	97.6	97.6	97.6	97.6	97.6	97.6	97.6	97.6	96.0	96.0
	Score	124	124	124	124	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	121	119	119
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B34964 S12412	S12418 S78056 PT0370	S31604 S78051 S54225	S54231 S54248 S54236	S54226 S54232 S09711 S13519
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117	120	135 135	139 140 141	141 142 146 147
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119	118	118	118	118 118 118
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ALIGNMENTS

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Greesies: Howo saplems (man)
C;Species: Howo saplems (man)
C;Species: Howo saplems (man)
C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C;Date: 13-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 20-Jun-2000
C;Accession: Szogol; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H) 4 germ-line genes.
A;Tetle: Polymorphism of human jmmunoglobulin V(H) 4 germ-line genes.
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: DNA
A;Status: DNA
A;Status: DNA
A;Status: DNA
A;Status: DNA
A;Status: DNA
A;Coss-references: UNIPARC:UPI0000116419; EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID
A;Cross-references: UNIPARC:UPI0000116419; EMBL:Z14237; NID:g37706; PIDN:CAA78606.1; PID
A;Title: The repartofre of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388

A;Accession: S26900 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-99 <TOM>

A;Cross-references: UNIPARC:UP10000116419; EMBL:Z12365; NID:g32948; PIDN:CAA78235.1; PIC C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-99/Domain: immunoglobulin homology <IMM>

Gaps ö Length 99; Indels Query Match
Best Local Similarity 100.0%; Pred. No. 6.8e-12;
Matches 25; Conservative 0; Mismatches 0;

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QVQLQESGPGLVKPSQTLSLTCTVS 25 δ 셤

RESULT 2

Igheavy chain V region - human C;Species: Homo sapiens (man) C;Accession: S26803 d. Requence_revision 13-Jan-1995 #text_change 20-Jun-2000 C;Accession: S26803 d. Vu. Lee, L.; Marcus, D.M. R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M. Eur. J. Immunol. 22, 1075-1082, 1992 A;Atitle: Polymorphism of human immunoglobulin V(H) 4 germ-line genes. A;Reference number: S26803 A;Accession: S26803 A;Accession: S26803 A;Accession: S26803 A;Accession: Lype: DNA A;Accession: S26803 A;Accession: S26803 A;Accession: S26803 A;Accession: S26803 A;Accession: S26803 A;Accession: S26803 A;Cross-references: UNIPARC:UPI0000116485; EMBL:Z14238; NID:g37710; PIDN:CAA78607.1; PI

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A;Cross-references: UNIPARC:UPI00004CF85; EMBL:Z14240; NID:g37712; PIDN:CAA78609.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;IS-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (DP-71 / VH 4.11 / 4.15) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26906; S09421; S12415
B;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
M;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V A;Reference number: S26885; MUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-97 < TOM>
A; Residues: 1-97 < TOM: UNIPARC: UP1000004CF81; EMBL: 212371; NID: 932962; PIDN: CAA78241.1; PID
A; Note: designated DP-71
R; Sanz, 1:; Kelly, P:; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
R; Sanz, 1:; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
A; Title: The smaller human V(H) gene families display remarkably little polymorphism.
A; Reference number: S09421; MUID: 90059975; PMID: 2511001
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C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 31-Dec-2004
C;Accession: PH0876
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C;Accession: S26804
R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Bur. J. Immunol. 22, 1075-1082, 1992
A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A;Reference number: S26800; MUID:92201299; PMID:1348029
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 97;
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Pred. No. 1.9e-11;
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A;Note: designated 4.11
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Pred. No. 1.9e-11;
1; Mismatches 0;
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Best Local Similarity 96.0%;
Matches 24; Conservative
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Best Local Similarity 96.0%;
Matches 24; Conservative
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A;Molecule type: DNA
A;Residues: 1-97 <SA2>
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A; Residues: 1-97 <SAN>
                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-97 < WEN>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C; Accession: 331585
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A; Reference number: 331585
A; Accession: 331585
C; Accession: 331585
A; Accession
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530534
Glaheavy chain V region - human
CjSpecies: Homo sapiens (man)
CjSpecies: Homo sapiens (man)
CjDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
CjAccession: S30534
RjMarlette, X.
Sibmitted to the EMBL Data Library, October 1992
A;Reference number: S30520
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                   Gaps
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                                                                                                                                          Length 99;
   C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>
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A;Cross-references: UNIPARC;UP10000113F45; EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterocetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IPM>
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                                                                                                                                   100.0%; Score 124; DB 2;
11arity 100.0%; Pred. No. 6.8e-12;
Conservative 0; Mismatches 0;
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Best Local Similarity
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Best Local Similarity
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A;Status: preliminary
A;Molecule type: mRNA
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S26804
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A;Cross-references: UNIPARC:UPI000011662A; EMBL:231383; NID:9472978; PIDN:CAA83258.1; PI C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-97/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GMl ganglioside IgM antibodies cloned from motor neuropa
A;Reference number: S57408
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A;Molecule type: mRNA
A;Residues: 1-115 < 49AT>
A;Cross-references: UNIPARC:UP100001137AD; EMBL:X87897; NID:9871273; PIDN:CAA61148.1; PI
                                                                                                                                                                                                                                                                                                                                                CjAccession: S44125
R; Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994
A; Reference number: S44105
A; Reference number: S44105
A; Accession: S44125
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C;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: B26340
R;Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                         Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
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Pred. No. 2.1e-11;
1; Mismatches 0; Indels
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Pred. No. 2.3e-11;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <1MM>
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R; Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison,
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  Similarity 96.0%; Pred. No. 2e-11; 24; Conservative 1; Mismatches
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1 Similarity 96.0%;
24; Conservative 1
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Best Local Similarity 96.0%;
Matches 24; Conservative i
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Best Local Similarity
Best Local Similarity
Matches 24; Conserv
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A; Residues: 1-105 < HAW>
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$12421
Ig heavy chain V region (4.22) - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Accession: 812421
R; Accession: 812421
R; Sanz, I: Really, P: Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
R; Sanz, I: Really b: Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
A; Title: The smaller human V(H) gene families display remarkably little polymorphism.
A; Reference number: 809421; WUD:90059975; PMID:2511001
A; Recession: 812421
A; Recession: S12421
A; Recession: S12421
A; Recession: S12421
A; Rededuce: 1-98 & SAN>
A; Readduce: 1-98 & SAN>
A; Recession: Immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology ciMM>
F; 15-98/Domain: immunoglobulin homology < NMM>
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R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B. J. Exp. Med. 174, 1639-1652, 1991
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype A;Reference number: PHO862; MUID:92078875; PMID:1660528
A;Reference number: PHO876
A;Rosselon: PHO876
A;Moles: 1-97 cMAN>
A;Residues: 1-97 cMAN>
A;Residues: 1-97 cMAN>
A;Rosser-references: UNIPROT:Q9UL73; UNIPARC:UPI0000176C0C
A;Note: the authors translated the codon TAT for residue 50 as Thr
A;Note: the authors translated by Epstein-Barr virus-transformed B cell that bears C;Superfamily: immunoglobulin homology
C;Roywords: heterotetramer; immunoglobulin
C;Superfamily: immunoglobulin homology cIMM>
F;15-97/Domain: immunoglobulin homology cIMM>
F;15-97/Domain: complementarity-determining 2
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Pred. No. 1.9e-11;
1; Mismatches 0; Indels
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Pred. No. 1.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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Best Local Similarity 96.0%;
Matches 24; Conservative
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Local Similarity 96.0%;
nes 24; Conservative
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Gaps

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Query Match

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1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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Job time : 21.2264 Becs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Accession: A26340
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$18557
Ig heavy chain V region precursor (VIV-4) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999
C;Accession: $18557
R;Shin, B.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, B.; F.
EMBO J. 10, 3641-3645, 1991
A;Title: Physicial map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Title: Physicial map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: $18557
A;Accession: $18557
A;Accession: $18557
A;Accession: $18557
A;Accession: $18557
A;Accession: $18557
A;Accession: $18557
A;Cross-references: UNIPARC:UPI0000115FF0; EMBL:X62112; NID:g37853; PIDN:CAA44022.1; PIL
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin predicted <SIG>F;20-116/Pomain: signal sequence #status predicted <AAT>F;20-116/Domain: immunoglobulin homology <IMM>
F;34-116/Domain: immunoglobulin homology <IMM>
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S20780
Ig heavy chain V region - human
C;Species: Homo saplens (man)
C;Decies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20780
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Reference number: S20764
A;Reference number: S20764
A;Reference number: S20764
A;Reference number: S20764
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-118 *AMOR>
A;Cross-references: UNIPARC:UP100001163F6; EMBL:Z11958; NID:g33893; PIDN:CAA78015.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>
A;Title: Organization and evolution of variable region genes of the human immunoglobuling A;Reference number: A26340; MUD:87051007; PMID:3097326
A;Reference number: B26340
A;Resesion: B26340
A;Residues: B26340
A;Residues: 1-116 < KOD>
A;Residues: 1-116 < KOD
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Pred. No. 2.3e-11;
1; Mismatches 0; Indels
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96.0%; Pred. No. 2.3e-11;
tive 1; Mismatches 0; Indels
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llarity 96.0%;
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Matches 24; Conservative
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Matches 24
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Rikodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T. C., Mol. Biol. 190, 529-541, 1986
A;Title: Organization and evolution of variable region genes of the human immunoglobulin A;Reference number: A26340; MID:87061007; PMID:3097326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPARC:UPI000011641A, EMBL:Z12366; NID:G32950; PIDN:CAA78236.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-118 <KOD>
A;Cross-references: UNIPARC:UPI000011B546; GB:M29811; NID:g185597; PIDN:AAC99493.1; PID:
A;Cross-references: UNIPARC:UPI000011B546; GB:M29811; NID:g185597; PIDN:AAC99493.1; PID:
A;Cross-references: UNIPARC:UPI000011B546; GB:Mcoss-references: UNIPARC:UPI00011B546; GB:Mcoss-references: UNIPARC:UPI00011B546; GB:Mcoss-references: Winter, G.
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of VA;Reference number: 826885; MUID:93021117; PMID:1404388
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C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A26340; S26901
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C;Keywords: heterotetramer; immunoglobulin
E;1-19/Domain: signal sequence #stetus predicted <SIG>
F;20-118/Product: Ig heavy chain V-II region 71-2 #status predicted <MAT>
F;30-118/Domain: immunoglobulin homology <IMA>
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       Length 118;
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   Score 121; DB 2;
Pred. No. 2.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                           Ig heavy chain precursor V-II region (71-2) - human
                                                                              1; Mismatches
                                                                                                                                                        1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                                                                   QVQLQESGPGLVKPSETLSLTCTVS 25
97.6%;
                                           Best Local Similarity 96.03
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA A; Residues: 20-118 <TOM>
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 25, 2006, 06:05:44 ; Search time 133.491 Seconds (without alignments) 132.131 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-764-428-2 124 1 QVQLQESGPGLVKPSQTLSLTCTVS 25

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 2166443 segs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

					SUMMARIES	
Regult No.	Score	Query Match	Length	DB	a	Description
1	124	100.0	476	2	Q6GMX1_HUMAN	ношо
8	124	100.0	478	~	Q7Z379_HUMAN	homo
m	121	97.6	119	0	Q9UL73_HUMAN	pomod .
4	121	97.6	139	~	Q86SX2_HUMAN	homo
ß	121	97.6	465	N	QGGMX6_HUMAN	pomod.
9	121	97.6	477	7	QGGMX7_HUMAN	OHOU.
7	121	97.6	620	N	Q96EY0_HUMAN	omod (
60	118	95.2	130	~	Q8IZD7_HUMAN	7 homo
σ	118	95.2	492	7	Q7Z374_HUMAN	_
10	116	93.5	477	~	Q510J1_RAT	rattu
11	115	92.7	117	-	HV2G HUMAN	omou s
12	115	92.7	122	7	Q9UL75 HUMAN	homo
13	114	91.9	150	7	095973_HUMAN	3 пошо
14	113	91.1	469	7	Q5M839_RAT	_
15	113	91.1	591	7	QSIOL9_RAT	rattu
16	112	90.3	478	7	Q6NYH3 HUMAN	рошо
17	112	90.3	576	~	Q6P4I8_HUMAN	
18	110	88.7	496	~	Q96KX8 HUMAN	_
19	110	88.7	590	~	Q569B8_RAT	
20	110	88.7	615	~	Q569B6_RAT	ratt
21	108	87.1	98	~	Q53VQ0 MOUSB	mus
22	108	87.1	98	N	Q53VQ4 MOUSE	mus m
23	108	87.1	98	••	Q53VQ8_MOUSE	mus mus
24	108	87.1	98	7	Q53VR2 MOUSE	MUB.
25	108	87.1	113	-	HV47 MOUSE	mu8
26	108	87.1	115	•	HV44 MOUSE	Enm
27	108	87.1	115	7	Q53VQ1 MOUSE	EUM.
28	108	87.1	116	-	HV60 MOUSE	BUM
29	108	87.1	119	~	Q53VQ5_MOUSE	mus .
30	108	87.1	119	7	Q53VQ9_MOUSE	BUB
31	108	87.1	119	~	Q53VR3_MOUSE	OS3vr3 mus musculu

Q99ng4 mus musculu P01824 homo sapien Q61bg5 mus musculu P01819 mus musculu Q65211 mus musculu Q99m22 mus musculu Q99m23 mus musculu Q81c63 homo sapien Q81c63 homo sapien Q81c53 mus musculu Q81c53 mus musculu Q53413 mus musculu Q53413 mus musculu Q53413 mus musculu Q53416 mus musculu
Q99NG4_MOUSE HV2F HUMAN GCERGE, MOUSE HV46_MOUSE HV43_MOUSE G55ZII_MOUSE G65ZII_MOUSE HV45_MOUSE HV62_MOUSE HV62_MOUSE HV62_MOUSE G9TG63_HUMAN GSM642_RAT HV61_MOUSE G5U413_MOUSE
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108 108 108 108 107 107 105 105
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# ALIGNMENTS

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Homo sapiens (human) (Fragment).
Homo sapiens (Human)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODL004YM19 of B cells (Ramos cell line) of
                                                                                                                                                                                                                                    Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2511001;
Sanz I., Kelly P., Williams C., Scholl S., Tucker P., Capra J.D.;
"The smaller human VH gene families display remarkably little
                                                                                        Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                      Diamond B.;
"Molecular characteristics of antibodies bearing an anti-DNA-
associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
NUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
MUX.Y. Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope; Submitted (FBB-2003) to the EMBL/GenBank/DDBJ databases. Submitted (FBB-2003) to the EMBL, BX248010; CAD62627.1; -; mRNA. HSSP; P01820; 1G7J. HSSP; P01820; 1G7J. SMR; QB6SXZ; 33-129. Ensembl; ENSG00000130076; Homo sapiens. InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=B cells;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 119 MW; 1BDB86B6420EA0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.6%; Score 121; DB 2;
96.0%; Pred. No. 1.1e-10;
iive 1; Mismatches 0
                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymorphism.";
EMBO J. 8:3741.3748(1989).
EMBI, AF035041; AAD56277.1; -; mRNA.
PIR; PH0876; PH0876.
PIR; S12416; S12416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P01820; 1G7J.
SMR; Q9UL73; 1-119.
InterPro: IPR007110; Ig-like.
InterPro: IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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0865XZ HUMAN

DG65XZ HUMAN PRELIMINARY;

AC 0865XZ;

DT 01-JUN-2003 (TrEMBLrel. 24,

DT 01-JUN-2003 (TrEMBLrel. 24,

DT 01-JUN-2003 (TrEMBLrel. 24,

DT 01-JUN-2003 (TrEMBLrel. 26,

DE Pull-length CDNA clone CSODI

DE HOMO sapiens (human) (Fragme

OC HOMO.

CE WARYOLA; Metazoa; Chordata

OC HOMO.

CO HOMO.

CO HOMO.

CO HOMO.

CO NCBI_TAXID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA LI W.B., GTUBER C., Jessee J

RI SUDMITTER (FRB-2003) to the

RN III W.B., GTUBER C., Jessee J

RL SUDMITTER (FRB-2003) to the

RN CLEOTIDE SEQUENCE.

RN GENGEODE;

RA GENOSCODE;

RA GENOSCODE;

RA GENOSCODE;

RA GENOSCODE;

RA SEMBL; BEX248300; CAD65627.1;

DR SNR, OGSCSZ, 33-1230.76;

DR DR SNR, OGSCSZ, 33-1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity ... Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
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Best Local Similarity
                                                                                                                                                                                                                PubMed=1660528
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NON TER
SEQUENCE
                                                                                                                        fetus.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapions (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUR-Human rectum tumor;
A Bloecker H., Beecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Beecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

R MSDP, PO1820; 1G7J.

R MSRP, PO1820; 1G7J.

R Brembl; ENSG0000130076; Homo sapiens.

R InterPro; IPR003507; 1g-1.

R Pfam; PF07554; C1-set; 2.

R Pfam; PF07554; C1-set; 2.
                                                                                                                                                Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 124; DB 2; Length 478; 100.0%; Pred. No. 1.6e-10; ive 0; Mismatches 0; Indels C
                                                                                                  Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                              0; Indels
PROSITE, PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 AA; 51620 MW; 4APCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothettoal protein DKFZp686K04218 (Fragment).
Name=DKFZp686K04218;
                                                                                        100.0%; Score 124; DB 2;
1larity 100.0%; Pred. No. 1.6e-10;
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                            478 AA.
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                                                                                                                                                                                                                     20 QVQLQESGPGLVKPSQTLSLTCTVS 44
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                                                                                                                                                                                            1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                                                                                                                                          PRT;
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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Q9UL73;
                                                                                                                                                                                                                                                                                                                                                       Q72379 HUMAN PRELIMINARY, Q72379;
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1es 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
NON TER 1
SEQUENCE 478 AA; 5
                                                                    NUCLEOTIDE SEQUENCE.
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NCBL_TaxID=9606;
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RESULT 3
49UL73 HU
10 09UL73 HU
AC 09UL
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Gaps

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Length 119; 0; Indels

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1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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QGGMX7 HU
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X Structuring Section 1.2477932; DOI=10.1073/pnas.242603899;

X Structuber R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Riaushers R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Boares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratchius R.W., Touchman J.W., Green B.D., Dickeon M.C.,

Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.B.,

Benerch A., Schein J.B., Jones S.J.M., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                      Gaps
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                                                                                                                        Score 121; DB 2; Length 139;
Pred. No. 1.2e-10;
1; Mismatches 0; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386B CRC64;
                                                                                     139 AA; 15573 MW; 7D1B2302410B4F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                465 AA.
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GO; GO:0016021; C:integral to membrane; IEA.
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InterPro; IPR001359; Ig.
InterPro; IPR00110; Ig-11ke.
InterPro; IPR00359; Ig_c1.
InterPro; IPR003596; Ig_W.
InterPro; IPR003596; Ig_W.
InterPro; IPR004596; Ig_W.
InterPro; IPR004596; Ig_W.
InterPro; IPR00409; Ig_ 2.
INTERPRO; IRC; 2.
INTERPRO; IRC; 3.
INTERPRO; IRC; 1.
INTERPRO; 1.
INT
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                                                                                                                                                                                                                  1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PSC9035; IG_LIKE; 1.
MON TER 1
                                                                                                                                                  96.0%;
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                                                                                                                                 97.6%;
                                                                                                                    Query Match
Best Local Similarity 96.0<sup>1</sup>
....hes 24; Conservative
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Q6GMX6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                      NON TER
SEQUENCE
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RX FUCLEUL SUPCENTE.

RX TISSUE=Primary B-Cells,

RX TISSUE=Primary B-Cells,

RX STRUBBEST, PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Klausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hägeh F.,

RA Diatchenko L., Maruaina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.W.,

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu K., Glibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhetsley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. "Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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Query Match
97.6%; Score 121; DB 2; Length 465;
Best Local Similarity 96.0%; Pred. No. 4.6e-10;
Matches 24; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 protein.
477 AA; 51631 MW; 9PB59C09C50CFF85 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotherical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477 AA
                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                                                                                                                                                                 20 QVQLQESGPGLVKPSETLSLTCTVS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 HUMAN
QGGMX7 HUMAN PRELIMINARY;
QGGMX7;
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SEQUENCE 47
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QVQLQESGPGLVKPSETLSLTCTVS 44

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MEDLINE-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A trausberg R.D., Colling F.S., Wargner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
A piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A piatchenko L., Warusina K., Farmer A.A., Rubin G.M., Scheefer T.E.,
Bromstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glabs R.A.,
A Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glabs R.A.,
A Whiting M., Madan A., Youchman J.W., Green B.D., Dickson M.C.,
Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski W.I., Skalska U., Smailus D.E.,
Connect A., Schein J.B., Jones S.J.M., Marra M.A.;
Connect D.N., Marra M.A.,
                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neale G.A., Kitchingman G.R.; mRNA transcripts initiating within the human immunoglobulin mu heavy
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                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
   620 AA.
      PRT;
                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26, IGHM protein.
Q96EYO HUMAN PRELIMINARY;
Q96EYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLECTIDE SEQUENCE.
TISSUE-Primary B-Cells;
NIH MGC Project;
                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686C0218 (Fragment).
Name-DKFZp686C02218;
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                  Gapa
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

HSSP, PO1820; 1G7J.

SWR; Q72374; 262-470.

SWR; Q72374; 262-470.

InterPro; IPR007110; 19-11ke.

InterPro; IPR003597; 19_21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 130;
   DB 2; Length 620;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-thyroglobulin heavy chain variable region (Fragment).
                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                             Jang Y.-J., Chung J., Park J.-Y., Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY145445; AAN64329.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AA; 13901 MW; 036131FC6EC1551E CRC64;
 Score 121; DB 2;
Pred. No. 6.3e-10;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.2%; Score 118; DB 2; 92.0%; Pred. No. 3.4e-10;
                                                                                                                                                                           130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              SMR; Q81ZD7; 1-130.
Ensembl; ENSG00000130076; Homo sapiens
                                                               1 QVQLQESGPGLVKPSQTLSLTCTVS 25
                                                                              OVOLORSGPGLVKPSETLSLTCTVS 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; 1GV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Query Match 97.6%;
Best Local Similarity 96.0%;
Matches 24; Conservative 1
                                                                                                                                                             77 HUMAN
QEIZD7 HUMAN PRELIMINARY;
QBIZD7;
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Q72374;
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SEQUENCE
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.D., Collins F.S., Wagner L., Shammen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibh F.N.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heibh F.,

B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Brownstein M.J., Usdin T.B., Toolhyuki S., Carninci P., Prange C.,

R. Richards S., McChan F.D., McKernan K.J., Malany S.J.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Helton D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,

R. Halton D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,

R. Halton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smailus D.E.,

R. Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smailus D.E.,

R. Ageneration and initial analysis of more than 15,000 full-length human

R. T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 95.2%; Score 118; DB 2; Length 492; Local Similarity 92.0%; Pred. No. 1.4e-09; nes 23; Conservative 2; Mismatches 0; Indels
                                                                                                                                                          492 AA; 53776 MW; 1B7A15760F0CA74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       477 AA
                                                                                                                                                                                                                                                                                      Created)
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PR07654; C1-8et; Z.
SMART; SM00406; IGv;
PROSITE; PS00390; IG_IKR; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00409; IG; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       QSIOJI_RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                         Hypothetical protein.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
OS10J1 RAT
OS10J1 RAT
OS10J1 RAT
DT 10-MAY,
DT 10-MAY,
DT 10-MAY,
DT 10-MAY,
DT 10-MAY,
DG 10-MAY,
DG 110-MAY,
DG 110-MAY,
DG 110-MAY,
DG 110-MAY,
DG 110-MAY,
DG 110-MAY,
DG Namme=10
OC NAMME=10
OC NAMME=10
OC NAMME NA
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
110 havy chain V-II region NEWM.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A90404; GIHUNM.

R PDB; TRAB; X-ray; H=2-117.

R SMR; P01825; 2-117.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0005955; P:immure response; NAS.

DR InterPro; IPR003196; Ig-like.

DR InterPro; IPR003196; Ig-like.

DR RART; SM00406; IGV; 1.

DR RART; SM00406; IG ILKE; 1.

DR PROSTER; PSS035; IG ILKE; 1.

DR PROSTER; PSS035; IG ILKE; 1.

DR RAMINOGLOBULIN V region; Pyrrolidone carboxylic acid.

TOWAIN

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Pyrrolidone carboxylic acid.
                                                                                                                                                                             Gapa
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Saul F.A., Amzel L.M., Poljak R.J.;
saul F.A., Amzel L.M., Poljak R.J.;
"preliminary refinement and structural analysis of the Pab fragment from human immunoglobulin new at 2.0-A resolution.";
J. Biol. Chem. 253:585-597(1978).
-j. MISCELLANBOUS: This chain was isolated from an IgG1 myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
-!- SIMILARITY: Contains 1 1g-like (immunoglobulin-like) domain.
                                                                                                                                                                             ö
                                                                                                                   Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=77242302; PubMed=407927; Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.; Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.; Andino acid sequence of the VH region of a human myeloma immunoglobulin (IgG New) "; Biochemistry 16:3412-3420(1977).
                                                                                                                                                                             Indels
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 477 AA; 52167 MW; 226460762898C6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT
                                                                                           Score 116; DB 2; Le
Pred. No. 2.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA.
                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                       1 QVQLQBSGPGLVKPSQTLSLTCTVS 25
                                                                                                                                                                                                                                                                  20 QVQLKESGPGLVQPSQTLSLTCTVS 44
                                                                                                                         93.5%;
                                                                                                                      Query Match
Best Local Similarity 92.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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P01825;
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150 AA
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HSSP, P01820; 1674.
SMR; 095973; 20-147.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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PROSITE; PS50835; IG_LIKE; 1.
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095973;
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hes 22; Conservative
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PIR; S78056; S78056.
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NUCLEOTIDE SEQUENCE.
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NCBI_TaxID=9606;
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Logtenberg T., Young F.M., Van Es J.H., Gmelig-Meyling F.H., Alt F.W.;
"Autoantibodies encoded by the most Jh-proximal human immunoglobulin
heavy chain variable region gene.";
J. Exp. Med. 170:1347-1355(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Bird J., Galili N., Link M., Stites D., Sklar J.;
Continuing rearrangement but absence of somatic hypermutation in immunoglobulin genes of human B cell precursor leukemia.";
J. Exp. Med. 168:229-245(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=2117273;
Schroeder H.W. Jr, Wang J.Y.;
"Preferential utilization of conserved immunoglobulin heavy chain
variable gene segments during human fetal life.";
Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88277139; PubMed-9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                           DB 1; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                                                                                                                                                                                                                                                          12790 MW; 2DA47B509562D237 CRC64;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                           92.7%;
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Q9UL75;
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nes 22; Conservative
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                                                                                                                                                                                                                                                                                          117 AA;
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SEQUENCE
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Harindranath N., Goldfarb I.S., Ikematsu H., Burastero S.E., Wilder R.L., Notkins A.L., Casali P.;
"Complete sequence of the genes encoding the VH and VL regions of low-and high-affinity monoclonal IgM and IgAl rheumatoid factors produced by CD5+ B cells from a rheumatoid arthritis patient."; Int. Immunol. 3:865-875(1991).
EMBL: AF103795; AAC79084.1; -; mRNA.
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Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2094 (TrEMBLrel. 26, Last annotation update)
VH4 heavy chain variable region precursor (Fragment).
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88.0%; Pred. No. 9.4e-10;
tive 2; Mismatches 1;
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Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Rischul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Rah Expleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Repleton M., Soares M.B., Bonaldo M.P., Carannor T.L., Scheetz T.E.,
Repleton M., Soares M.B., Ronaldo M.P., Carannor T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rohards B., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren R.J., Lu X., Glbbs R.A.,
Richards B., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren R.J., Lu X., Glbbs R.A.,
Rahes J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Rahiting M., Madan A., Young A., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B. J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A., Schein J.E., Jones B.J.M., Marra M.A.,
R. Hands A.,
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
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Potential.
VH4 heavy chain variable region.
                                                                                                                                Length 150;
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Director MGC Project;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC088254; AAH88254.1; -; mENA.
GO; GO:0003823; P:antigen binding; IRA.
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51403 MW; 030A2C3C66228F16 CRC64;
  1 19 Potential.
20 >150 WH4 heavy chain variable:
150 150 WW, 85664E0493BAA7C9 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                          Score 114; DB 2;
Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                              469 AA
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InterPro; IPR007110; IG-11ke.
InterPro; IPR003597; IG.1.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_W.
Pfam; PF07654; Cl_Bet; 3.
                                                                                                                          91.9%;
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PROSITE; PS00290; IG_MHC; UNR
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                                                                                                                    Query Match
Best Local Similarity 88.0°
                                                                                                                                                                                                                                                                                                                                                                                                                         QSM839 RAT PRELIMINARY;
QSM839;
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SEQUENCE
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1058839 PAH
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Length 469;

DB 2;

91.1%; Score 113;

Query Match

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Bukaryota; Metazos; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;

Muridae; Murinae; Rattus.
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NIH MGC Project;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC081184; AAH88184.1; -; MRNA.
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                                                                                                                                                                   10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
LOC366747 protein (Fragment).
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88.0%; Pred. No. 1.1e-08;
iive 3; Mismatches 0;
Best Local Similarity 88.0%; Pred. No. 8.3e-09;
Matches 22; Conservative 3; Mismatches 0
                                                                                                                                                     591 AA.
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                                                             SMART; SM00409; IG; 2.
SMART; SM00407; IGG: 4.
SMART; SM00408; IGC: 2.
SMART; SM00406; IGV: 1.
PROSITE; PS50835; IG LIXE; 5.
PROSITE; PS00290; IG MHC; UNKNOWN_3.
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InterPro; IPR007110; Ig-like.
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InterPro; IPR003598; Ig_C2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Pfam; PF07654; C1-set; 4.
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Best Local Similarity 68.0%
Matches 22, Conservative
                                                                                                                     RESULT 15
Q510L9_RAT
ID Q510L9_RAT PRELIMINARY;
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Search completed: April 25, 2006, 06:24:43 Job time : 134.491 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                    April 25, 2006, 06:58:17; Search time 108.962 Seconds (without alignments) 95.866 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/uS07_PUBCOMB.pep:*

; /cgn2_6/ptodata/1/pubpaa/uS08_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/uS108_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
; /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-783-950-137
US-10-994-9608-219
US-10-984-9608-219
US-10-171-681-19
US-10-171-680-19
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US-10-453-698-82
US-10-029-926B-90
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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28 124 100.0 99 4 US-10-379-392-45 Sequence 45, Appl 29 124 100.0 99 4 US-10-379-392-46 Sequence 46, Appl 30 124 100.0 99 5 US-10-379-392-46 Sequence 47.8 Appl 31 124 100.0 107 3 US-10-309-762-74 Sequence 74, Appl 32 124 100.0 110 5 US-10-309-762-74 Sequence 77, Appl 34 124 100.0 110 5 US-10-310-513-5 Sequence 27, Appl 36 124 100.0 117 4 US-10-310-613-5 Sequence 1, Appl 37 124 100.0 117 4 US-10-310-513-5 Sequence 1, Appl 39 124 100.0 117 4 US-10-310-530-5 Sequence 13, Appl 39 124 100.0 117 4 US-10-530-530-5 Sequence 13, Appl 40 124 100.0 117 4 US-10-660-357-5 Sequence 13, Appl 41 124 100.0 117 5 US-10-660-357-13 Sequence 5, Appl 41 124 100.0 117 5 US-10-660-357-13 Sequence 5, Appl 41 124 100.0 118 4 US-10-078-7578-50 Sequence 13, Appl 41 124 100.0 118 4 US-10-078-7578-50 Sequence 138, Appl 44 124 100.0 118 4 US-10-084-103-43 Sequence 25, Appl 44 124 100.0 118 4 US-10-684-313-8 Sequence 25, Appl 45 124 100.0 118 4 US-10-684-313-8 Sequence 25, Appl 45 124 100.0 118 4 US-10-684-313-8 Sequence 25, Appl 45 124 100.0 118 4 US-10-684-313-8 Sequence 25, Appl 45 124 100.0 118 4 US-10-684-313-8 Sequence 25, Appl 45 124 100.0 118 4 US-10-684-313-8 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 119 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence 25, Appl 45 124 100.0 118 4 US-10-30-43 Sequence
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## ALIGNMENTS

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RESULT 1

US-10-764-428-2

Sequence 2, Application US/10764428

Publication No. US20040229310A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
TITLE OF INVENTION: CULTURE
CURRENT FILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: US 60/442,484

PRIOR PRING DATE: 2003-01-23

NUMBER OF SEQ ID NOS: 33

SOUTHARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 25
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Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 25; Conservative 0; Mismatches 0;
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Publication No. US20050042664A1

GENERAL INFORMATION:

APPLICANT: Wu, Herren

APPLICANT: Dall'Acqua, William

APPLICANT: Damschroder, Melissa

TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES

FILE REFERENCE: AE60UMBER: US/10/923,068

CURRENT APPLICATION NUMBER: US/10/923,068

CURRENT APPLICATION NUMBER: US/10/923,068

CURRENT FILING DATE: 2004-08-20

NUMBER OF SEQ ID NOS: 518

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 381

LENGTH: 25
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ORGANISM: Artificial Sequence
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US-10-923-068-381
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  25; Conservative
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ORGANISM: Homo sapiens
US-10-783-950-137
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ORGANISM: Homo sapien
US-09-563-222-146
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US-10-923-068-249
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                                                                                                                                                                                                                                                                  Sequence 28, Application US/09874141

| Publication No. US20030012781A1
| Publication No. US20030012781A1
| GENERAL INFORMATION:
| APPLICANT: ANDERSON, DARRELL
| APPLICANT: PAN, LI-ZHEN
| APPLICANT: RASTETTER, WILLIAM S.
| APPLICANT: RASTETTER, WILLIAM S.
| APPLICANT: RASTETTER, WILLIAM S.
| APPLICANT: ALORIZER, WILLIAM S.
| TITLE OF INVENTION: NON-ACONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
| TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
| FILE REFERENCE: 037003-0280632
| CURRENT FILING DATE: 2001-06-06
| PRIOR FILING DATE: 2000-06-06
| PRIOR FILING DATE: 2000-06-06
| NUMBER OF SEQ ID NOS: 53
| SOFTWARE: PATENTIN VET. 2.1
| SEQ ID NO 28
| LENGTH: 30
| TENGTH: 30
| TENGTH: 30
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Sequence 29, Application US/09874141

Publication No. US2030012781A1

GENERAL INFORMATION:

APPLICANT: ANDERSON, DARRELL

APPLICANT: PAN, LI-ZHEN

APPLICANT: HANNA, NABLL

APPLICANT: RASTETTER, WILLIAM H.

APPLICANT: KLOETZER, WILLIAM S.

TITLE OF INVENTION: NON-AGONISTIC ANTHEODIES TO HUMAN GP39, COMPOSITIONS

TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF

FILE REFERENCE: 037003-0280632

CURRENT APPLICATION NUMBER: US/09/874,141

CURRENT FILING DATE: 2000-06-06

PRIOR FILING DATE: 2000-06-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 29

LENGTH: 30
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                                                                Query Match
100.0%; Score 124; DB 5;
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 25; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 25; Conservative
    ; ORGANISM: Homo sapiens
US-10-923-068-381
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; ORGANISM: Homo sapiens
US-09-874-141-29
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Sequence 137, Application US/10783950

Publication No. US20040199945A1

GENERAL INFORMATION:

APPLICANT: EPICYTE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

CURRENT APPLICATION NUMBER: US/10/783,950

CURRENT FILING DATE: 2004-02-19

PRIOR PILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 182

SEQ ID NOS: 182

SEQ ID NO 37

TENTOR DATE: DATE: DATE: 2000-05-02

SEQ ID NO 37
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                                                                                                                                                                                 Sequence 146, Application US/09563222
Publication No. US20030079253A1
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: BURARYOTIC CELLS
TITLE OF INVENTION: 2000-05-02
CURRENT PAPLICATION NUMBER: US/09/563,222
CURRENT PAPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SEQ ID NO 146
LENGTH: 30
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1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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CURRENT FILING DATE: 2004-11-08
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US-10-171-681-19
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Fublication No. US20050142137A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chui, Daniel
APPLICANT: Chord, Haihong
APPLICANT: Chord, Haihong
APPLICANT: Ara, Gulehan
APPLICANT: Lakochelle, William J.
TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
TITLE OF INVENTION: ANTIBODIES AGAINST
FILE REFERENCE: Cura 970
CURRENT APPLICATION NUMBER: US/10/984,960A
CURRENT PILLING DATE: 2004-11-08
FRIOR PILLING DATE: 2004-11-07
NUMBER OF SEQ ID NOS: 112
SOFTRARE: Curasequist version 0.1
SEQ ID NO 21
LENGTH: 30
LENGTH: 30
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LENGTH: 30
LENGTH: 30
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Publication No. US20050142137A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gallo, Michael
APPLICANT: Shong, Halhong
APPLICANT: Ara, Gulshan
APPLICANT: LaRochelle, William J.
APPLICANT: LaRochelle, William J.
APPLICANT: LAROCHELLE ANTHEODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
FILE REPERRENCE: Cura 970
CURRENT APPLICATION NUMBER: US/10/984,960A
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100.0%; Score 124; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                           APPLICANT: WL. Herren
APPLICANT: Walliam
APPLICANT: Dall'Acqua, William
TITLE Damschroder, Melissa
TITLE NOF INVENTION: HUMANIZATION OF ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 30
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     Sequence 249, Application US/10923068
Publication No. US20050042664A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT

GRGANISM: Homo sapiens
US-10-923-068-249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-10-984-960A-57
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US-10-171-681-19
US-10-171-681-19
US-10-171-681-19
Sequence 13, Application US/10171681
Sequence 13, No. US203017023341
Sequence 14, Application US. US203017023341
Septicant One. US203017023341
APPLICANT: BLACK, Amelia
APPLICANT: NEWAN, Nabil
APPLICANT: NEWAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9D39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9D39,
TITLE OF INVENTION: HOMANIZED ANTIBODIES TO HUMAN 9D39,
TITLE OF INVENTION: Doane, Swecker & Mathis
STREET: P.O. Box 1404
STREET: P.O. Box 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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100.0%; Score 124; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/518,275
PRIOR PLING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 57
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-10-984-960A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVQLQESGPGLVKPSQTLSLTCTVS
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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US-10-171-680-20
US-10-171-680-20
Sequence 20, Application US/10171680
Sequence 20, Application Wo. US20030175269A1
Sequence 20, Application Wo. US20030175269A1
Septicant: BLACK, Amelia
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: NEWNAN, Roland A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUTTB, Doane, Swecker & Mathie
COMPOSITIONS CONTAINING AND THERAPEUTIC USB THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 87;
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                                NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis STREET: B.O. 600x 1404

CITY: Alexandria STREET: P.O. 600x 1404

CITY: Alexandria STATE: Virginia COUNTRY: United States
ZIP: Z2313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATER: IBM PC COMPATIBLE OF SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/171,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTAY: United States
ZIP: 22313-1404
COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 124; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-2021
TELEFRAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OVOLORSGPGLVKPSQTLSLTCTVS 25
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APPLICATION NUMBER: US/08/554,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/332,595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWANAN, ROLAIDA A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Sequence 19, Application US/10171680
Sequence 19, Application US/10171680
PUBLICACION NO. US20030175269A1
GENERAL INFORMATION:
APPLICANT: HANNA, Nabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9p39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF INVENTION: CURECLAIMS

NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis STRET: P.O. Box 1404
CITY: ALexandria
CONTRY: Urginia
CONPUTRY: Urginia
COMPUTRY: INFO Compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
FILING DATE: 17-UNB-2001
CLASSIFICATION NUMBER: US/08/925,339
FILING DATE: O7-NOV-1995
ATTORNEY ABENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION:
TELEBRONE: (703) 836-2620
TELESPAN: (703) 836-2021
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH CATION APPLICATIOS
LENGTH CATION APPLICATIOS:
LENGTH CATION APPLICATION INFORMATION:
TELEBRONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH CATION APPLICATION
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                     QVQLQBSGPGLVKPSQTLSLTCTVS 25
                                                                              QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                                       Sequence 20, Application US/10171681 Publication No. US20030170233A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 25; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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Gaps

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Search completed: April 25, 2006, 07:08:49 Job time : 109.962 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGULT 15
US-10-194-975-38
US-10-194-975-38

§ Sequence 38, Application US/10194975
§ Publication No. US20030039649A1

§ GENERAL INFORMATION:

§ APPLICANT: Foote, Jefferson

§ TITLE OF INVENTION: Super Humanized Antibodies

§ CURRENT APPLICATION NUMBER: US/10/194,975

§ CURRENT FILING DATE: 2002-10-10

§ PRIOR APPLICATION NUMBER: US 60/305,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-10-194-975-36

Sequence 36, Application US/10194975

Publication No. US20303039649A1

GENERAL INPORMATION:

APPLICANT: FOOCE, Jefferson

TITLE OF INVENTION: Super Humanized Antibodies

FILE REPERENCE: 501231.01

CURRENT PILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: US/10/194,975

CURRENT FILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 122

SEQ ID NOS: 122

SEQ ID NO 36

LENGTH: 99
                   FILING DATE:
CLASSIFICATION
FILING PAPELCATION DATA:
APPLICATION NUMBER: 09/332,595
FILING DATE:
APPLICATION NUMBER: 08/654,840
FILING DATE:
APPLICATION NUMBER: 05/030
FILING DATE:
ATOCNEY AGENT INPORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
FELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION SA6-620
INPORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 anno acids
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APPLICATION NUMBER: US/10/171,680
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: maino acid
STRANDEDNESS: single
TOPOLOGY: linear
SMOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-194-975-36
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                                                                                                                                                                                                                                                                             1 OVOLORSGPGLVKPSOTLSLICTVS 25
; PRIOR FILING DATE: 2001-07-12; NUMBER OF SEQ ID NOS: 122; SOFTWARE: Patentin version 3.1; SEQ ID NO 38; LENGTH: 99; TYPE: PR T Mmo sapiens US-10-194-975-38
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April 25, 2006, 07:01:21 ; Search time 16.0377 Seconds (without alignments) 68.593 Million cell updates/sec
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1. /SIDS5/ptodata/1/pubpaa/USO8 NEW FUB.pep:*
2. /SIDS5/ptodata/1/pubpaa/USO5*NEW FUB.pep:*
3. /SIDS5/ptodata/1/pubpaa/PCT_NEW FUB.pep:*
4. /SIDS5/ptodata/1/pubpaa/PCT_NEW FUB.pep:*
5. /SIDS5/ptodata/1/pubpaa/US10 NEW FUB.pep:*
6. /SIDS5/ptodata/1/pubpaa/US10 NEW FUB.pep:*
7. /SIDS5/ptodata/1/pubpaa/US10 NEW FUB.pep:*
8. /SIDS5/ptodata/1/pubpaa/US11_NEW FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Blocceleration Ltd.
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124
1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARIE

121 97.6 97 7 US-II-054-669-42 121 97.6 97 7 US-II-054-669-51 121 97.6 97 7 US-II-054-669-52 121 97.6 97 7 US-II-054-669-52 121 97.6 97 7 US-II-084-554-54 121 97.6 97 7 US-II-084-554-54 121 97.6 97 7 US-II-144-222-36 121 97.6 97 7 US-II-114-222-44 121 97.6 97 7 US-II-1136-250-53 121 97.6 97 7 US-II-1136-250-54 121 97.6 97 7 US-II-1182-343-44 121 97.6 99 7 US-II-012-35-74 121 97.6 99 7 US-II-012-35-74 121 97.6 99 7 US-II-012-35-47 121 97.6 99 7 US-II-012-35-47 121 97.6 99 7 US-II-012-55-55 121 97.6 99 7 US-II-014-59-47 121 97.6 108 6 US-II-0935-005B-36 121 97.6 108 6 US-II-0935-005B-36 121 97.6 108 6 US-II-0935-005B-36 121 97.6 108 7 US-II-0135-005B-36 121 97.6 108 7 US-II-01935-005B-36 121 97.6 108 7 US-II-01935-005B-36 121 97.6 108 7 US-II-061-821-6	Sequence 42, Appl Sequence 51, Appl Sequence 52, Appl	Sequence 54, Appl Sequence 36, Appl Sequence 44, Appl Sequence 44, Appl		6, 4, 5, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6,	Sequence 36, Appl Sequence 6, Appli
	777	7 US-11	7 US-11 7 US-11 7 US-11 7 US-11	7 US-1 7 US-1 7 US-1 6 US-1	6 US
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## ALIGNMENTS

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Sequence 50, Application US/11084554

Publication No. US2005266679A1

GENERAL INFORMATION:

APPLICANT: Kellermann, Sirid-Ai

APPLICANT: Kellermann, Sirid-Ai

APPLICANT: Kellermann, Sirid-Ai

APPLICANT: Korver, Wouter

TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

TITLE OF INVENTION: ANTIBODIES THROUGH V GENB MANIPULATION

FILE REPERENCE: ABGENIX.100A

CURRENT PAPLICATION NUMBER: US/11/084,554

CURRENT PILING DATE: 2005-03-17

PRIOR PILING DATE: 2004-03-19

SOFTWARE: FREISE FOR WINGOWE VERSION 4.0

SOFTWARE: FREISE FOR WINGOWE VERSION 4.0
                                                                                                                 Query Match 100.0%; Score 124; DB 7; Length 99; Best Local Similarity 100.0%; Pred. No. 2.6e-11; Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                       US-11-054-669-39
Sequence 39, Application US/11054669
Sequence 39, Application US/11054669
Publication No. US2050261480A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 3019/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT PILING DATE: 2005-02-08
PRIOR FILING DATE: 2002-07-12
PRIOR PILING DATE: 2002-07-12
PRIOR PILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SEQ ID NO 39
LENGTH: 99
                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-38
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US-11-054-669-39
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ORGANISM: Homo sapiens
US-11-084-554-50
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US-11-004-590-42

US-11-004-590-42

Sequence 42, Application US/11004590

Publication No. U32006000883A1

GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazar, Gregory Alan
APPLICANT: Hammond, Phillip W.

ITILE OF INVENTION: CONTEXT AND COMPOSITIONS THEREOF
ITILE OF INVENTION: CONTEXT AND COMPOSITIONS THEREOF

ITILE REPERENCE: 18832/US/5

CURRENT APPLICATION NUMBER: US/11/004,590

CURRENT APPLICATION NUMBER: US 60/527,167

PRIOR PILING DATE: 2004-12-04

PRIOR PILING DATE: 2004-06-21

PRIOR APPLICATION NUMBER: US 60/619,483

PRIOR PILING DATE: 2004-10-14

NUMBER OF SEQ ID NOS: 458

SOFTWARE: Patentin version 3.3

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US-11-004-590-43

Sequence 43, Application US/11004590

Publication No. USZ006000883A1

GENERAL INFORMATION:

APPLICANT: Desjarlais, John R.

APPLICANT: Desjarlais, John R.

APPLICANT: Hammond, Phillip W.

TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF

FILE REFERENCE: 185832/US/5

CURRENT APPLICATION NUMBER: US/11/004,590

CURRENT FILING DATE: 2004-12-03

PRIOR FILING DATE: 2004-12-03

PRIOR FILING DATE: 2004-06-21

PRIOR FILING DATE: 2004-06-21

PRIOR FILING DATE: 2004-06-21

PRIOR PILING DATE: 2004-06-31

PRIOR PILING DATE: 2004-06-31

PRIOR PILING DATE: 2004-06-31

PRIOR PILING DATE: 2004-06-31

PRIOR PILING DATE: 2004-08-13

PRIOR PILING DATE: 2004-08-13
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QVQLQESGPGLVKPSQTLSLTCTVS 25
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; ORGANISM: Homo sapiens
US-11-004-590-42
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CRGANISM: Homo sapiens
US-11-004-590-43
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APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
                                                      Gaps
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Sequence 50, Application US/11136250

Publication No. US20060021074A1

GENERAL INFORMATION:

APPLICANT: Gleen, Larry L.

APPLICANT: Green, Larry L.

APPLICANT: Korver, Wouter

ITILE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

ITILE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION

FILE REFERENCE: ABGENIX.100A2

CURRENT APPLICATION NUMBER: 10/084,554

PRIOR PILING DATE: 2005-03-17

PRIOR PILING DATE: 2004-05-24

PRIOR PILING DATE: 2004-03-19

NUMBER OF SEQ ID NOS: 266

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 99
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Query Match 100.0%; Score 124; DB 7; Length 99; Best Local Similarity 100.0%; Pred. No. 2.6e-11; Matches 25; Conservative 0; Mismatches 0; Indels
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CURRENT PILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/755,916
PRIOR PILING DATE: 2003-12-16
PRIOR PLICATION NUMBER: PR 0308538
PRIOR PLICATION NUMBER: PR 0308538
PRIOR PLICATION NUMBER: PC/FR03/00178
PRIOR PLICATION NUMBER: PC/FR03/00178
PRIOR PLICATION NUMBER: PC/FR03/0179
PRIOR PLICATION NUMBER: PR 0205753
PRIOR PLICATION NUMBER: PR 0205753
PRIOR PLICATION NUMBER: PR 0205753
PRIOR FILING DATE: 2002-05-07
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Publication No. US20050249730A1
GENERAL INFORMATION:
APPLICANT: GOETSCH, LILIANE
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DUFLOS, ALAIN
HAEUW, JEAN-FRANCOIS
IEGER, OLIVIER
BECK, ALAIN
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; OKGANISM: Homo sapiens
US-11-136-250-50
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Best Local Similarity
Matches 25; Conserva
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APPLICANT:
APPLICANT:
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Sequence 237, Application US/11004590
Publication No. US2006000883A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OP INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OP INVENTION: CONTENT AND COMPOSITIONS THEREOF
CURRENT APPLICATION NUMBER: US/11/004,590
CURRENT PILING DATE: 2004-12-03
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100.0%; Score 124; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 25; Conservative 0; Mismatches 0; Indels (
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APPLICANT: OIKE, Shinsuke
APPLICANT: TAGAWA, TOSHIAKI
APPLICANT: HOSOKUMA, Saiko
APPLICANT: HOSOKUMA, Saiko
APPLICANT: HOSOKUMA, Saiko
TITLE OP INVENTION: Antibody recognizing antigen
FILE REFERENCE: 235054
FILE REPERENCE: 235054
PRIOR APPLICATION NUMBER: US/10/530,171
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: US/10/72003/012732
PRIOR APPLICATION NUMBER: US/2002-291953
PRIOR PILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 22
SOFTWARE PATENT NOS: 22
SOFTWARE PATENT NOS: 22
SOFTWARE PATENT NOS: 22
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100.0%; Pred. No. 3.2e-11;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                               LOCATION: (59)
CTHER INFORMATION: Variable amino acid
US-11-012-353-72
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PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO 72
LENGTH: 117
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Publication No. US20060057147A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-530-171-7
                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                       FEATURE:
NAME/KEY: MOD_RES
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US-11-004-590-237
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Sequence 342, Application US/11004590

Dublication No. US20660008883A1

Sequence 342, Application US/11004590

Dublication No. US20660008883A1

APPLICANT: Lazar, Gregory Alan

APPLICANT: Lazar, Gregory Alan

APPLICANT: Hammond, Phillip W.

TITLE OF INVENTION: CONTEXT AND COMPOSITIONS THEREOF

TITLE OF INVENTION: CONTEXT AND COMPOSITIONS THEREOF

FILE REFERENCE: 185932/US/5

CURRENT APPLICATION NUMBER: US/11/004,590

CURRENT APPLICATION NUMBER: US 60/527,167

PRIOR PILING DATE: 2004-12-03

PRIOR PILING DATE: 2004-06-21

PRIOR PILING DATE: 2004-06-21

PRIOR PILING DATE: 2004-06-13

PRIOR PILING DATE: 2004-10-14

NUMBER OF SEQ ID NOS: 458

SOFTWARE: Patentin version 3.3

SEQ ID NO 342

LENGHH: 119

LENGHH: 119
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CONTENT AND COMPOSITIONS THEREOF
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           TILLE REFERENCE: 185912/US/5
CURRENT APPLICATION NUMBER: US/11/004,590
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR PILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/601,665
PRIOR APPLICATION NUMBER: US 60/601,665
PRIOR PILING DATE: 2004-06-13
PRIOR FILING DATE: 2004-06-13
PRIOR FILING DATE: 2004-06-13
PRIOR FILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PATENT VERSION 3.3
SOFTWARE: PATENT VERSION 3.3
SOFTWARE: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic US-11-004-590-340
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                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial
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US-11-004-590-348
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Publication No. US20060008883A1

GENERAL INFORMATION:

APPLICANT: Lazar, Gregory Alan

APPLICANT: Desjarlais, John R.

APPLICANT: Hammond, Phillip W.

TILLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
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100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                            Length 119;
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100.0%; Score 124; DB 7;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0;
  PRIOR FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US 60/581,613
PRIOR PILING DATE: 2004-06-21
PRIOR PILING DATE: 2004-08-13
PRIOR PILING DATE: 2004-08-13
PRIOR FILING DATE: 2004-10-14
NUMBER: PRIOR FILING DATE: 2004-10-14
SOFTWARE: PATENTON NUMBER: US 60/619,483
SOFTWARE: PATENTON NUMBER: US 60/619,483
SOFTWARE: PATENTON NUMBER: US 60/619,483
                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLQESGPGLVKPSQTLSLTCTVS 25
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                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-237
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US-11-004-590-340
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     1 OVQLQESGPGLVKPSQTLSLTCTVS 25
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Sequence 348, Application US/11004590

Publication No. US20060008883A1

GENERAL INFORMATION:

APPLICANT: Lazar, Gregory Alan

APPLICANT: Desjarlais, John R.

APPLICANT: Hammond, Phillip W.

TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING

TITLE OF INVENTION: CONYENT AND COMPOSITIONS THEREOF

TITLE OF INVENTION: CONYENT AND COMPOSITIONS THEREOF

TITLE OF INVENTION: CONYENT ADD COMPOSITIONS THEREOF

FILE REFERENCE: 185832/US/5

CURRENT APPLICATION NUMBER: US 60/527,167

PRIOR PILING DATE: 2004-10-0-3

PRIOR PILING DATE: 2004-06-21

PRIOR PILING DATE: 2004-06-21

PRIOR PILING DATE: 2004-06-13

PRIOR APPLICATION NUMBER: US 60/601,665

PRIOR PILING DATE: 2004-08-13

PRIOR PILING DATE: 2004-08-13

PRIOR APPLICATION NUMBER: US 60/601,665

PRIOR PILING DATE: 2004-10-14

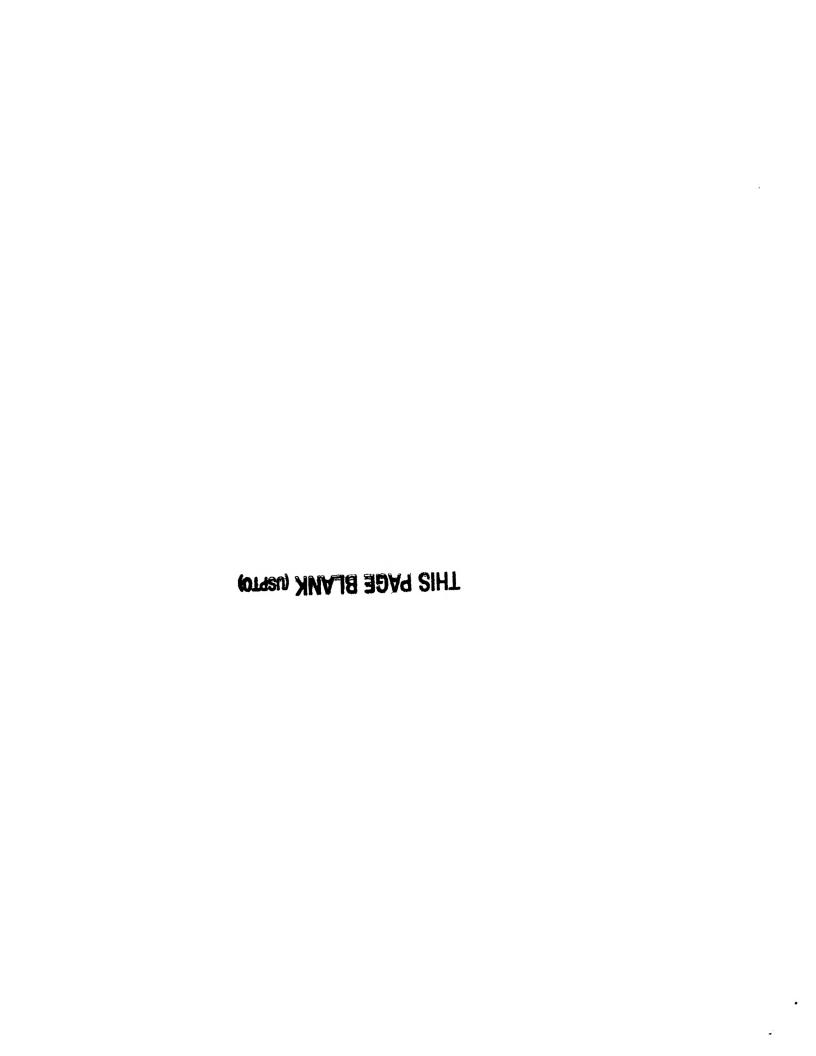
NUMBER OF SEQ ID NOS: 458

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LEVEL ARROTH: 119
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APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjarlais, John R.
APPLICANT: Hammond, Phillip W.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: MUMBER: US 11/004,590
CURRENT APPLICATION NUMBER: US 60/527,167
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR PLILING DATE: 2004-06-21
PRIOR PRILING DATE: 2004-06-31
PRIOR PRILING DATE: 2004-06-31
PRIOR PRILING DATE: 2004-06-31
PRIOR PRILING DATE: 2004-06-31
PRIOR PRILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 458
SEQ ID NO 352
LENGTH: 119
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100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 124; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
CTHER INFORMATION: Synthetic US-11-004-590-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Synthetic US-11-004-590-348
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ORGANISM: Artificial
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US-11-004-590-352
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April 25, 2006, 06:05:16 ; Search time 133.491 Seconds (without alignments) 82.286 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Blocceleration Ltd.
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1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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Gapop 10.0 , Gapext 0.5
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geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* geneseqp20008:* geneseqp20018:* geneseqp1980s:* geneseqp1990s:* Post-processing: Minimum Match 0% Maximum Match 100 Listing first 45 A_Geneseq_21:* **Database**:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

SUMMARIES

Human ant Human ant Human ant Human ant Human ant Human ant Adq92397 Human hul Adq80586 Human hea Anti-VEGP Human ant Mouse Human Human Human Human Human Human Human Human Human Description Add90699 Add31531 Add31531 Add31531 Add31483 Add31489 Add31489 Add31384 Add31399 Add31399 Add31395 Add31357 Add31353 Add931357 Add931357 Add931357 Add931359 ADY31534 ADY31516 ADY31351 ADY31399 ADY31483 4DX27037 4DY31384 ADY31402 4AB19691 80 Length Query 88 8 8 80 Score Result

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Tumour necrosis factor alpha; TNF-alpha mediated disease;
sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;
neurodegenerative disease; malignancy; TNF-secreting tumour;
neurodegenerative disease; malignancy; TNF-secreting tumour;
alcohol-induced hepatitis; psoriasis; psoriatic arthritis;
wegener's granulomatosis; ankylosing spondylitis; heart failure;
wegener's granulomatosis; ankylosing spondylitis; heart failure;
wegener's granulomatosis; hepatitis C infection; Kawasaki's pathology;
wegener's promonery taxis; telangiectasia; Alzheimer's disease;
westsum's disease; ataxis; telangiectasia; Alzheimer's disease;
Nown's syndrome; parkinson's disease; leukaemia; myelodygpastic syndrome;
wegener, alcorative colitis; amyotrophic lateral sclerosis;
wellple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;
shy-drager syndrome; cachexia; infectious disease; antibody therapy;
wenultiple sclerosis; Grave's disease; antibody therapy;
whuman; heavy chain variable region; VH; FR; framework region. Huse WD; Marquis D, ADQ92397 standard; peptide; 25 AA. 08-JAN-2003; 2003US-00338627. 08-JAN-2003; 2003US-00338627 Watkins JD, Vasserot AP, (first entry) Human hul FRH1 peptide (WATK/) WATKINS J D. (VASS/) VASSEROT A P. (MARQ/) MARQUIS D. WPI; 2004-524894/50. (MARQ/) MARQUIS D (HUSE/) HUSE W D. US2004131613-A1. Homo sapiens. 23-SEP-2004 08-JUL-2004 ADQ92397; ADQ92397 

New composition comprising a tumor necrosis factor alpha (TNF-alpha)

N-PSDB; ADQ92401

Human

AEC20858

4EB13673

Human Human

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binding polypeptides and their encoding polymoclectides. The invention is useful for treating TNR-alpha mediated disease such as sepsis, an autoimmune disease, rheumatoid arthritis, inflammatory diseases, an autoimmune disease, rheumatoid arthritis, inflammatory diseases, conversed and alignate pathologies involving TNR-secreting tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthritis, wester failure, conversed secreting tumours, alcohol-induced hepatitis, psoriatic arthritis, conversed secreting traperfusion injury, chronic obstructive pulmonary disease, pulmonary fibrosis, hepatitis C infection, Kawasaki's pathology, Refsum's disease, parkinson's disease, leukaemias (acute, chronic myelocytic, chronic lywphocytic and/or myelodyspastic syndrome), lymphomas (Hodgkin's, non-Hodgkin's and Euckitt's syndrome), hypokinetic movement disorders, drug-induced movement disorders, crohn's disease, ulcerative colitis, amyotrophic convented disorders, multiple sclerosis, Grave's disease, diabetes consistent and infectious diseases. The invention is also useful in antibody therapy. The present sequence is human hul framework sub-region of heavy chain variable (VH) cregion (FRH) peptide. This sequence is used in the invention.
                                                                                                                                 present invention relates to tumour necrosis factor alpha (TNF-alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNF-alpha binding; complementarity determining region; CDR; TNF-alpha; immunoassay; CDRL-3; CDRH-3; sepsis; autoimmune disease; rheumatoid arthritis; allergy; multiple sclerosis; systemic lupus erythematosus; scleroserma; diabetes mellitus; cachexia; parasitic disease; infectious disease; sarcoidosis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; allerative colitis; Crohn's disease; Alzheimer, s disease; Down's syndlation; Parkinson's disease; Wegener's disease; Down's syndlation; paoriasis; ankylosing spondylitis; Wegener's granulomatosis; idiopathic pulmonary fibrosis; asthma; graft-versus-host disease; leukemia; human.
binding molecule, useful for treating a TNF-alpha mediated disease such as sepsis, an autoimmune disease, rheumatoid arthritis, and neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 123; DB 8; Length 2:
100.0%; Pred. No. 4.7e-10;
tive 0; Mismatches 0; Indels
                                                                                       Disclosure; SEQ ID NO 65; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human heavy chain framework region FR1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ80586 standard; peptide; 25 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JAN-2003; 2003US-00338552.
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Best Local Similarity 100.
Matches 25, Conservative
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VASSEROT A P.
MARQUIS D.
HUSE W D.
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(VASS/)
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(HUSE/)
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The invention relates to a composition which comprises a TNP-alpha binding molecule having sequence of complementarity determining region (CDR) in 1940t chain variable region (CDR)-3 and sequence of CDR in composition is useful in the heavy chain variable region (CDR)-3. The composition is useful in the treatment of TNP-alpha mediated diseases. TNP-alpha binding molecule is useful for treating sepsis, autoimmune disease, rhematoid arthritis, allery, multiple sclerosis, systemic lupus erythematosus, scleroderma, diabetes mellitus, cachexia, acute and chronic parasitic and/or infectious diseases, sarcoidosis, inflammatory bowel disease, ulcerative colitis, Crohn's disease, disseminated intravascular coagulation, parkinson's disease, Alzheimer's disease, Down's syndrome, psoriasis, ankylosing spondylitis, Wegener's granulomatosis, idiopathic pulmonary fibrosis, asthma, graft-versus-host disease, or leukemia. TNF-alpha binding molecule is useful in diagnostic methods for detecting TNF-alpha in a sample. The present sequence detecting or quantifying TNP-alpha in a sample. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antibilitalmantory; antiangiogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; antiogenic disorder; immunological disorder; anti-VBGF antibody; antibody; heavy chain; FR1. anti vascular endothelial cell growth factor antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-VEGF antibody heavy chain FR1 subgroup III peptide SEQ ID NO:3.
                                                                                         Composition useful for treating diseases such as leukemia, asthma, rheumatoid arthritis, Alzheimer's disease, psoriasis or multiple sclerosis, comprises TNF-alpha binding molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 123; DB 8; Length 25; 100.0%; Pred. No. 4.7e-10; ive 0; Mismatches 0; Indels
Vasserot AP, Marquis D, Huse WD;
                                                                                                                                                                       Disclosure; SEQ ID NO 65; 60pp; English.
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                                    WPI; 2004-516978/49.
N-PSDB; ADQ80590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 AA;
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 Watkins JD,
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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.

WPI; 2005-180802/19.

Disclosure; SEQ ID NO 339; 179pp; English

The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework

DNA library; humanized antibody; antibody engineering; heavy chain. Human antibody heavy chain framework peptide - SEQ ID 339. ADY31507 standard; peptide; 25 AA 22-AUG-2003; 2003US-0497213P. 13-OCT-2003; 2003US-0510741P. 20-AUG-2004; 2004US-00923068 (MEDI-) MEDIMMUNE INC. US2005042664-A1. Homo sapiens 05-MAY-2005 24-FEB-2005 ADY31507; Wu H, RESULT 4 ADY3150 合 ઠે

DNA library; humanized antibody; antibody engineering; heavy chain.

US2005042664-A1

24-PBB-2005.

Homo sapiens

Human antibody heavy chain framework peptide - SEQ ID 363.

(first entry)

05-MAY-2005

ADY31531;

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ADY31531 standard, peptide; 25

RESULT 5 ADY31531 ID ADY3

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antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprises expressing a variable domain of the antibody or antigen binding fragment variable domain crecovering the antibody or antigen binding fragment variable domain crecovering the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid the method described above has a substitution of at least one amino acid position with a different amino acid, where the different amino acid is the amino acid found at the corresponding FR position of a human subgroup convariable domain consensus sequence that has a hypervariable region!

(HYRI) and/or HYRZ amino acid sequence with the most sequence identity with a corresponding HYRI and/or HYRZ sequence of the variable domain.

(HYRI) and/or HYRZ amino acid sequence of the variable domain.

(HYRI) and/or HYRZ amino acid sequence of the variable domain.

(C) The antibody or antigen binding fragment The antibody and antigen binding fragment in antibody and antigen immunomodulatory activities, and can be used in antibody and antigen methods and compositions of the present invention are useful for methods and compositions of the present invention are useful for the prevention are included the contraction of antique the contraction of a the present invention are useful for the prevention antident or antidention of a the prevention of a producing antident or antidention of the present invention are useful for the prevention of the present invention are useful for the prevention antidention of the present invention are useful for the prevention of the preven
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                                                                                                     Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes a method for producing an antibody or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
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100.0%; Score 123; DB 8;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                             Claim 15; SEQ ID NO 3; 161pp; English.
WPI; 2004-562149/54.
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1 EVOLVESGGGLVQPGGSLRLSCAAS 1 EVQLVESGGGLVQPGGSLRLSCAAS

Match 100.0%; Score 123; DB 9; Local Similarity 100.0%; Pred. No. 4.7e-10; les 25; Conservative 0; Mismatches 0;

Sequence 25 AA;

peptide.

Query Match

Matches

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Length 25;

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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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13-OCT-2003; 2003US-0510741P.
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(first entry)

Sequence 25 AA;

Damschroder M;

Dall-Acqua W,

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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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    DNA library; humanized antibody; antibody engineering; heavy chain.
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; Pred. No. 4.7e-10;
0; Mismatches 0;
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13-OCT-2003; 2003US-0510741P.
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Best Local
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        Score 123; DB 9;
Pred. No. 4.7e-10;
; Mismatches 0;
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Pred. No. 4.7e-10;
100.0%; Score ... . 7e-
100.0%; Pred. No. 4.7e-
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13-OCT-2003; 2003US-0510741P.
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      Query Match
Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity
Matches 25; Conserv
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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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                                                                                              The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework
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                                                                                                                                                                                                                                                                     Length 25;
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                                                                                                                                                                                                                                                                    100.0%; Score 123; DB 9; 100.0%; Pred. No. 4.7e-10;
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                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                    Disclosure, SEQ ID NO 315; 179pp; English
                                                                                                                                                                                                                                                                                                                                   1 EVQLVESGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Damschroder M;
                                                                                                                                                                                                                                                                                                                                                        FVQLVESGGGLVQPGGSLRLSCAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADY31489 standard; peptide; 25
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Matches 25; Conservative
                                                                                                                                                                                                                                                                                                      25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-180802/19
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 AA;
                                                                                                                                                                                                                                        Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ношо варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADY31489;
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                                                                                                                                                                                                                                                                                      Best Loc
Matches
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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                            DNA library; humanized antibody; antibody engineering; heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
                                                                                                                                                                                                                                                                                                                          Human antibody heavy chain framework peptide - SBQ ID 372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse 3A6 antibody heavy chain, N-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 123; DB 9;
Pred. No. 4.7e-10;
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                                     1 EVQLVESGGGLVQPGGSLRLSCAAS
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                                                                                                                                                                           ADY31540 standard; peptide; 25 AA
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100.0%; Pr
tive 0;
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13-OCT-2003; 2003US-0510741P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2004; 2004US-00923068
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                                                                                                                                                                                                                                                                                05-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Humanised antibody; interleukin-5; IL-5; recombinant antibody; antibody engineering; monoclonal antibody; MAb; 39D10; CDR; complementarity determining region; heavy chain; framework; eosinophilia;

allergy; asthma

Human group III heavy chain framework 1.

(first entry

25-JUN-1996

AAR87049;

AAR87049 standard; peptide; 30 AA

RESULT 12

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The invention relates to binding molecules (SEQ ID Nos 2 and 3) capable of binding to human NegoA polypeptide (SEQ ID No: 5), human NiG polypeptide (SEQ ID No: 5), human NiG comparison of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retinopathy, age-related macular degeneration, or pathologic myopia. This sequence represents the N-terminal sequence of the heavy chain of mouse 3A6 antibody as determined by sequence degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New binding molecule capable of binding to human NogoA polypeptide, human NiG-D20, or human NogoA342-357, useful for treating nerve repair, Alzheimer's disease, Parkinson's disease, or amyotrophic lateral
ocular disease; diabetic retinopathy; age related macular degeneration; myopia; cns-gen; neuroprotective; nootropic; antiparkinsonian; antidiabetic; ophthalmological; 3A6.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitaliti A;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwab ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 30; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mir AK,
                                                                                                                                                                                                                                                  17-SEP-2004; 2004WO-EP010489.
                                                                                                                                                                                                                                                                                                 19-SEP-2003; 2003GB-00021997.
                                                                                                                                                                                                                                                                                                                                            (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Frentzel S,
                                                                                                                                                                                                                                                                                                                                                                                                (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-242564/25
                                                                                                                                                   WO2005028508-A2
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                                                                                                      Mus musculus
                                                                                                                                                                                                     31-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                             Barske C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sclerosis
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Anti-human IL-5 recombinant antibody - useful for preventing or reducing eosinophilia and for treating certain allergic diseases, esp. asthma.

(CLLT ) CELLTECH THERAPEUTICS LTD.

95WO-GB001411. 94GB-00012230.

16-JUN-1995; 17-JUN-1994;

W09535375-A1 Homo sapiens

28-DEC-1995.

Bodmer MW, Athwal DS,

Emtage JS,

WPI; 1996-058412/06.

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                                                                                                                                                                                                                                                                                                                                                                                            Framework regions (AAR87049-52) of human group III (gp3) germ line antibody heavy chain showed homology to corresponding regions (AAR87053-56, respectively) of the rat anti-human interleukin-5 monoclonal antibody 39D10 heavy chain (see AAR87039). This homology was utilised in the prodn. of a humanised 39D10 VH (AAR87058) in which rat 39D10 VH complementarity determining regions were grafted into the human gp3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR; complementarity determining region; rheumatoid; osteo-arthritis; sepsis; congestive heart failure; shock; tissue transplant; tuberculosis; AIDS; Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome; cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis; inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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100.0%; Pred. No. 5.6e-10;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE19691 standard; peptide; 30 AA
                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 4; 69pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Gaps

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100.0%; Score 123; DB 9; Length 29; 100.0%; Pred. No. 5.4e-10; ive 0; Mismatches 0; Indels

1 EVQLVESGGGLVQPGGSLRLSCAAS 25 EVQLVESGGGLVQPGGSLRLSCAAS 25

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25; Conservative

Best Local Similarity Matches 25; Conserv

Query Match

Thomas K,

Mclaughlin J,

sv, 유

Gustafson M,

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29-JUL-2004; 2004WO-IB002529
                                                                    08-AUG-2003; 2003US-0493740P
                                                                                                 (PHAA ) PHARMACIA CORP
                                                                                                                                                          WPI; 2005-152548/16.
               17-PEB-2005.
                                                                                                                               Banerjee A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antibody molecule having specificity for human tumour necrosis factor-alpha (TNFalpha) comprising a heavy or light contains the antibody or the compound comprising the antibody is useful for treating or manufacturing a medicament for treating a pathology mediated treating or manufacturing a medicament for treating a pathology mediated by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha mediated confesses which can be treated by the antibody include sepsis, congestive heart failure, septic or endotoxic shock, cacharda, adult respiratory distress syndrome, septic or endotoxic shock, cacharda, adult respiratory distress syndrome, acquired immunodeficiency syndrome (AIDS), allergies, confessis, inflammatory bone disorders, blood coagulation disorders, burns, rejection episodes following organ or tissue transplant, crohn's disease and autoimmune diseases, such as thyroiditis. The antibodies may also be used to reduce the side effects associated with TNFalpha generation during neoplasty therapy, to eliminate or reduce shock-related symptoms associated with the treatment or prevention of shock-related symptoms associated with the treatment or prevention of shock-related symptoms associated with the treatment or prevention of states and allure, or in the diagnosis and imaging of disease states involving elevated levels of TNF alpha. The present sequence is human compared to the companion of the invention compared to the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                             New antibody specific for human tumor necrosis factor (TNF)-alpha, useful for treating TNF-alpha-mediated diseases, e.g. congestive heart failure, septic or endotoxic shock, cachexia, adult respiratory distress syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human group 3 consensus heavy chain framework region peptide - SEQ 106.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody; antiarthritic; antirheumatic; gastrointestinal-gen.; antiinflammatory; rheumatoid arthritis; musculoskeletal disease; inflammatory bowel disease; gastrointestinal disease; inflammation; Crohns disease; immune disorder; heavy chain.
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   neoplasty therapy; immunomodulator; vulnerary; graft rejection.
                                                                                                                                                                                                        Weir ANC, Popplewell AG, Chapman AP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 30;
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100.0%; Pred. No. 5.6e-10;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADX27037 standard; peptide; 30 AA
                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 2; 119pp; English
                                                                                                                    05-JUN-2001; 2001WO-GB002477.
                                                                                                                                                 06-JUN-2000; 2000GB-00013810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                              (CELL-) CELLTECH R & D LTD
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Matches 25; Conservative
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                                                                                                                                                                                                                                                    WPI; 2002-216732/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30 AA;
                                                              WO200194585-A1
                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-2005
                                                                                           13-DEC-2001
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                                                                                                                                                                                                                           King DJ;
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The invention relates to a novel method for preparing an antibody with a cheavy and light chain comprising fermenting a cell mixture, where the cells are capable of expressing the light and heavy chain, separating the cells are capable of expressing the light and heavy chain, separating the cells are capable of expracting the light and producing the pellet to stand for a hold time, extracting the cell pellet, allowing the pellet to cells from the supernatant to for the invention demonstrates antiatrinite, antirheumatic, gastrointestinal-gen. and antiinflammatory activities and may be useful for treatment of rheumatoid arthritis or an inflammatory bowel disease, such as Crohn's disease. Currently used anti-TNR-alpha monoclonal continuation and etanercept, have limited success in the treatment of disease since they must be administered frequently or intravenously. Furthermore, both of these molecules comprise large contraints and as such are difficult and expensive to manufacture. The proteins and as such are difficult and expensive to manufacture. The current sequence is that of a human group 3 consensus heavy chain current sequence antibody targeted to TNR-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Preparing a tumor necrosis factor-alpha antibody having a heavy and light chain comprises fermenting a cell mixture, forming a cell pellet and allowing the pellet to stand for a hold time.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA library; humanized antibody; antibody engineering; heavy chain.
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100.0%; Pred. No. 5.6e-10;
ive 0; Mismatches 0;
                                                                                                                                                        Example 4; SEQ ID NO 106; 125pp; English.
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Matches 25; Conservative
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New library of nucleic acid sequences comprises nucleotide sequences encoding humanized heavy chain variable regions and humanized light chain variable regions, useful for producing humanized antibodies.
                                                                                                                                                                                                                   The invention comprises a library of nucleotide sequences encoding humanized antibody heavy chain variable regions and humanized antibody light chain variable regions. The library of the invention is useful for producing humanized antibodies, or for re-engineering or reshaping an antibody from a first species for use in a second species. The present amino acid sequence represents a human germline heavy chain framework peptide.
                                                                                                                                                                           Disclosure; SEQ ID NO 216; 179pp; English
Wu H, Dall-Acqua W, Damschroder M;
                                       WPI; 2005-180802/19.
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1 BVQLVESGGGLVQPGGSLRLSCAAS 25 1 EVQLVESGGGLVQPGGSLRLSCAAS 25 ઠ 셤

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Gaps

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100.0%; Score 123; DB 9; Length 30; 100.0%; Pred. No. 5.6e-10; tive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100.0 Matches 25; Conservative

Sequence 30 AA;

Search completed: April 25, 2006, 06:15:08 Job time : 134.491 secs

Tue Apr 25 08:25:48 2006

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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model 38 - protein search, using OM protein

April 25, 2006, 06:15:41; Search time 21.2264 Seconds (without alignments)
[13.322 Million cell updates/sec Run on:

US-10-764-428-3 123

1 EVQLVESGGGLVQPGGSLRLSCAAS 25 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

1	heavy	Ig heavy	Ig heavy	Ig heavy	heavy chain V	Ig heavy	Ig heavy chain V-	Ig heavy	Ig heavy	heavy	Ig heavy	heavy	heavy chain	Ig heavy chain	heavy	Ig heavy chain	Ig heavy	heavy chain -	heavy chain V-	heavy chain -	heavy chain V-	heavy	Ig heavy chain -	heavy chain	Ig heavy	Ig heavy ch	781 Ig variable reg	557 Id heavy ch	
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ery	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	000	3
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Ig variable region Ig heavy chain V r Ig heavy chain pre	Ig heavy chain pre Ig heavy chain V r Ig heavy chain V r	heavy heavy heavy	heavy heavy heavy	ig neary chain pre Ig heavy chain pre Ig heavy chain V-I Ig heavy chain V r
137780 JL0048 B28966	C34964 S26889 S54856	PL0122 S25571 H3HUTL	AIHUTU GIHUWS H3HU26	A45953 B34964 M3HUPM D36005
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## ALIGNMENTS

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	(DP-48)
	To heavy chain V region
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	chain
ULT 1	Pe 9 5
RESULT	9 0

C;Species: Homo sapiens (man) C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

CjAccession: S26890
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26895, MUID:93021117; PMID:1404388
A;Recession: S26890
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <TOM>

A;Cross-references: UNIPARC:UP100001138FA; EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PIC C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-97/Domain: immunoglobulin homology <IMM>

Gaps õ Length 97; Indels Query Match
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 25; Conservative 0; Mismatches 0;

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# 1 EVQLVESGGGLVQPGGSLRLSCAAS 25 1 EVQLVESGGGLVQPGGSLRLSCAAS 25

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Ig heavy chain V region (YAC-5) - human

C.Species: Homo sapiens (man) C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Wisture Genet. 7, 162-168, 1994 A;Title amp of the human immunoglobulin V(H) locus completed by analysis of the teloman A;Reference number: 846460; MUID:95004581; PMID:7920635 A;Accession: 846462

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-97 <COO>

A; Cross-raferences: UNIPARC: UP100001165D9; EMBL: Z27504; NID: 9505430; PIDN: CAA81824.1; P: C; Superfamiler: immunoglobulin V region; immunoglobulin v region; immunoglobulin C; Keywords: heterotetramer; immunoglobulin P;15-97/Domain: immunoglobulin homology < IMM>

Gaps ö Length 97; IndelB Query Match 100.0%; Score 123; DB 2; Best Local Similarity 100.0%; Pred. No. 3.7e-10; Matches 25; Conservative 0; Mismatches 0;

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1 EVQLVESGGGLVQPGGSLRLSCAAS 25

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A;Cross-references: UNIPARC:UP10000116412; EMBL:Z17392; NID:g32840; PIDN:CAA78996.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;IS-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (DP-59) - human (fragment)
Cispecies: Homo sapiens (man)
Cipate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
CiAccession: 526934
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
Nol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: $26885; WUID:93021117; PMID:1404388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UD1000116415; EMBL:Z12359; NID:g32937; PIDN:CAA78229.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;IS-98/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0123; S26897
B;Bird, J; Gallli, N.; Link, M.; Stites, D.; Sklar, J.
J; Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A;Reference number: PL0123
A;Accession: PL0123
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F;15-98/Domain: immunoglobulin homology < IMM.
F;31-35/Region: complementarity-determining 1
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A; Residues: 1-98 «BIR»
A; Cross-references: UNIPARC: UPI0000116413
A; Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A; Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement
A; Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement
A; Tomlinaon, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A; Reference number: $26885; MUID:93021117; PMID:1404388
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; Pred. No. 3.8e-10;
0; Mismatches 0;
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   A; Molecule type: DNA
A; Residues: 1-98 <TOM>
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A; Residues: 1-98 <TOM>
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Best Local 8
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                                                                                                                                                                               In heavy chain V-III region (TD-Vp) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Statili, N.; Link, M.; Stites, D.; Sklar, J.
N; Blrd, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 166, 229-245, 1988
A; Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulir
A; Reference number: PL0116; MUID:88286083; PMID:2840480
A; Accession: PL0121
A; Molecule type: mRNA
A; Residues: 1-98 *BIR>
A; Cross-references: UNIPARC:UP10000176897
A; Cross-references: UNIPARC:UP10000176897
A; Cross-references: D cells from patient TD with acute lymphoblastic leukemia, ALL
A; Note: the sequence shows the V region; immunoglobulin homology
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology *IMM>
F; 15-98 Domain: immunoglobulin homology *IMM>
F; 15-98 Domain: complementarity-determining 1
F; 49-65/Region: complementarity-determining 2
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226894
Ig heavy chain V region (DP-51) - human (fragment)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Accession: 826894
CiAccession: 826894
RiTomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
A; Tile: The repertoire of human germline V(H) sequences reveals about fifty groups of A; Reference number: 826885; MUID:93021117; PMID:1404388
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Ig heavy chain V region (COS 6) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29545
R;Tomlinson, M:; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Reference number: S29543
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100.0%; Pred. No. 3.8e-10;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-98 < TOM>
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26933
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPARC:UP1000011640D; EMBL:Z12340; NID:g32902; PIDN:CAA78210.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
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R; Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-7798, 199
A; Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A; Reference number: 826885; MUID:93021117; PMID:1404388
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A;Residues: 1-100 <TON>
A;Residues: 1-100 <TON>
A;Cross-references: UNIPARC:UPI0000116407; EMBL:Z12332; NID:g32883; PIDN:CAA78202.1; PI:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups A;Reference number: S26885; MuID:93021117; PMID:1404388
A;Accession: S26926
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (DP-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0;
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Pred. No. 3.8e-10;
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100.0%; Pred. No. 3.8e-10;
ative 0; Mismatches 0;
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100.0%; Score 123; D
Best Local Similarity 100.0%; Pred. No. 3.8
Matches 25; Conservative 0; Mismatches
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Best Local Similarity 100.0
Matches 25; Conservative
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A;Residues: 1-100 <TOM>
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826891
Ig heavy chain V region (DP-58) - human (fragment)
C;Species: Home saplens (man)
C;Species: Home saplens (man)
C;Species: Home saplens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: 12691
A;Attle: The repertoire of human germline V(H) sequences reveals about fifty groups of VA;Reference number: 826881
A;Reference number: 826881
A;Accession: $26891
A;Accession: $26891
A;Realus: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>A;Residues: 1-98 <TOM>A;Residues: 1-98 <TOM>A;Coss-references: UNIPARC:UP10000116414; EMBL:Z12358; NID:g32935; PIDN:CAA78228.1; PIL
C;Superfamily: immunoglobulin vegion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
D; Mol. Biol. 227, 776-798, 1992
D; Mol. Biol. 227, 776-798; Mol. 1992
D; Mol. Biol. 227, 776
D; Mol. Biol. 227, 776-798; Mol. 1992
D; Mol. Biol. 227, 776-798; Mol. 1992
D; Mol. Biol. 227, 776-798; Mol. 1992
D; Mol. Biol.
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S26933
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Species: Homo sapiens (man)
Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
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Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                     Length 98;
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; Pred. No. 3.8e-10;
0; Mismatches 0;
                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-10;
Matches 25; Conservative 0; Mismatches 0;
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                                         P;49-65/Region: complementarity-determining 2
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Best Local Similarity 100.0%;
Matches 25; Conservative 0
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826933
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S36280
Ig heavy chain V region (clone alpha-FOG1-A3) - human (fragment)
C;Species: Home sapiens (man)
C;Decies: Home sapiens (man)
C;Decies: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Decessions: 335280
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Ttle: Human anti-self antibodies with high specificity from phage display libraries.
A;Accessions: S36280
A;Access
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S17079
IG heavy chain V-gene (clone HHG19) - human
C; Species: Homo saplens (man)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C; Accession: S60299; S17079
R; Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
R; Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A; Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm
A; Reference number: S60299
A; Accession: S60299
A; Scaleus: preliminary
A; Molecule type: DNA
A; Residues: 1-117 < KU2>
A; Residues: 1-117 < KU2>
A; Residues: 1-117 < KU2>
A; Residues: UNIPARC:UPI000115FF4; EMBL:X62128; NID:G38340; PIDN:CAA44059.1; PIL
A; Roces-references: UNIPARC:UPI000115FF4; EMBL:X62128; NID:G38340; PIDN:CAA44059.1; PIL
A; Roces-tics:
A; Introns: 16/1
C; Genetics:
A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology < IMM>
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C;Accession: 860295; 821996
R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm
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A; Reference number: $60295; MUD: 93122853; PMID: 1282498
A; Accession: $60295
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A; Cross-references: UNIPARC: UP10000115FP6; EMBL: X62130; NID: 938344; PIDN: CAA44061.1; PID
A; Cross-references: UNIPARC: UP10000115FP6; EMBL: X62130; NID: 938344; PIDN: CAA44061.1; PID
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology < IMM>
C; Keywords: heterotetramer; immunoglobulin
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(Fragment).
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE-98277139; PubMed-9614934; DOI-10.1006/clin.1998.4531;
MEDLINE-98277139; PubMed-9614934; DOI-10.1006/clin.1998.4531;
MEDLINE-98277139; PubMed-9614934; DOI-10.1006/clin.1998.4531;
Young D.C.;
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01-WAY-2000 (TrEMBirel. 13, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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      STTWENT BENEVATION OF THE STANFILL OF THE STAN
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21-JTL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 heavy chain V-III region TEI.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
Diamond B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=155592;
Makiya R., Stigbrand T.;
Placental alkaline phosphatase has a binding site for the human immunoglobulin-G Fc portion.";
Fur. J. Blochem. 205:341-345(1992).
EMBL; AR035023; AAD56259.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.";
J. Exp. Med. 174:1639-1652(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 123; DB 2; 100.0%; Pred. No. 1.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
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MEDLINE=74142702; PubMed=4522793;
Capra J.D., Kehoe J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig.v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Conservative
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PIR; S21205; S21205.
PIR; S30531; S30531.
HSSP; P01783; ILGC.
SWR; Q9UL91; 1-117.
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ID HV3P HUMAN
AC P01777;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last amnotation update)
1g heavy chain V-III region BRO.
1g heavy chain V-III region BRO.
Bukaryota, Metacoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metacoa; Chordata, Craniata, Primates, Catarrhini; Hominidae,
Mammalia, Butheria; Burchontoglires, Primates, Catarrhini; Hominidae,
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Immunochemistry 13:995-999(1976).
-|- MISCELLANEOUS: This chain was obtained from IgM isolated from the serum of a patient with malignant lymphoma of the Waldenstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
"Variable region sequences of five human immunoglobulin heavy chair of the VH3 subgroup: definitive identification of four heavy chain hypervariable regions "0.8.A. 71:845-848(1974).
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MEDLINE=77117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
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                                                                                                                                                                                                                      -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
-!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
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PROSITE; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular region; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:000555; P:iamune response; NAS. InterPro; IPR007110; Ig-like.
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Best Local Similarity 100.
Matches 25; Conservative
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HSSP; P01772; 2FB4.
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119 AA;
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SMR; P01766; 1-120.
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Query Match
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Q6MZV6_HU
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                    100.0%; Score 123; DB 1; Length 120; 100.0%; Pred. No. 1.8e-09; cive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                      120 120 120 1327 MW; D3F0428F7C2E6410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005955; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SNART; SM00406; IGV; 1.
PROSITE; PSS0835; IG-LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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HSSP; P01861; 1ADQ.
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Interpro; IPR003109; Ig-11ke.
Interpro; IPR003597; Ig cl.
Interpro; IPR003006; Ig MHC.
Interpro; IPR003596; Ig v.
Pfam; PP07654; Cl-8et; 3.
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QEP181;
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NIH MGC Project;
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Best Local Similarity
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Name=IGHM;
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The German Human convertium;

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,

Submitted (AUG-2003) to the BMBL/GenBank/DDBJ databases.

REARL, BK40854; CA845921.1; -; mRNA.

RRSP, PO1842; 1AQK.

RRSP, 1AQK.

RRSP, 1AQK.

RRSP, 12-10-11 in RNA.

RRSP, 11-10-11 in RNA.

RRSP, 11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo saplens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 7.2e-09;
Matches 25; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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479 AA; 51639 MW; 6FA495DF0AA71DD4 CRC64;
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGV; I.
PROSITE; PS00290; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 478 AA; $\overline{5}2667 MW; 17\overline{1}8238D917970D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-UTL-2004 (TrEMBLrel. 27, Created)
05-UTL-2004 (TrEMBLrel. 27, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothettal protein DKFZp686L19235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 123; DB 2;
100.0%; Pred. No. 7.2e-09;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVOLVESGGGLVQPGGSLRLSCAAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, IGHAl protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGGMX2_HUMAN PRELIMINARY;
QGGMX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76_HUMAN
QGMZV6_HUMAN PRELIMINARY;
QGMZV6;
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QEMZV7_HUMAN PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                         116
49
54
68
84
116
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SMR; P19181; 20-116.
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24;
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                                                                                                                                                 Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Stanefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Stanefer C.P., Bhat N.K.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldow M.P., Carninci P., Frange C.,
B. Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton B.K. Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakebley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Blakebley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length human
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                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 47, Last sequence update)
10-NAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V region 5A precursor.
Carassius auratus (Goldfish).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BC073771, AA473771.1; -; mRNA.
EMBL, BC073771, AA473771.1; -; mRNA.
EMBL, BC073771, AA473771.1; -; mRNA.
InterPro; IPR003599; Ig.
InterPro; IPR003109; Ig.c1.
InterPro; IPR003596; Ig.mc.
InterPro; IPR003596; Ig.v.
PF00554; C1-set; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 123; DB 2;
100.0%; Pred. No. 7.4e-09;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
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25; Conservative
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            Homo sapiens (Human).
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                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissum=Spleen
Name=IGHA1;
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Best Local &
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686C11235.
Name-DKFZp686C11235;
Name-DKFZp686C11235;
Name-DKFZp686C11235;
Macmayota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
NUCLEOTIDE SEQUENCE.
MEDILINE=8814476; PubMed=3125551;
MEDILINE=88014476; PubMed=3125551;
Wilson M.R., Middleton D., Warr G.W.;
"Immunoglobulin heavy chain variable region gene evolution: structure and family relationships of two genes and a pseudogene in a teleost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Blocker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (JAN1-2005) to the EMBL/GenBank/DDBJ databases.

R EMBL; BX640853; CAE45920.1; -; mRNA.

R Interpro; IPR003599; Ig.

R Interpro; IPR003599; Ig.

R Interpro; IPR003597; Ig.cl.

R Interpro; IPR003597; Ig.cl.

R Interpro; IPR003596; Ig.WHC.

R Interpro; IPR003596; Ig.WHC.

R SMART; SM00409; IG.2.

R SMART; SM00409; IG.2.

R SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR07110; 1g-like.
InterPro; IPR031596; 1g_v.
SMART; SM00406; 1Gv; 1Gv; 1.
PR051TE; PS06135; 1G LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12808 MW; 9C2279E2DF199B12 CRC64;
                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.2%; Score 122; DB 1; 96.0%; Pred. No. 2.4e-09;
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TISSUE-Small intestine;
The German CDNA Consortium;
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Ig heavy chain V-III region TIL.
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Best Local Similarity 96.0
Matches 24; Conservative
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                                                                                                                                          PROTEIN SEQUENCE.
                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Restricted utilization of germ-line VH3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo saplens (Human)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=1730252;
Raaphorst P.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
Schuurman R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
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MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 113;
                                                                                                    99.2%; Score 122; DB 2; Length 473; 96.0%; Pred. No. 9.9e-09; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      DI-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.6%; Score 120; DB 2; Length 11 Best Local Similarity 96.0%; Pred. No. 4.5e-09; Matches 24; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AA; 12437 MW; ED57FDD19086D07F CRC64;
    PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 473 AA; 52121 MW; 9476EAR4C0BFC447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
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(Rel. 01, Last sequence update)
(Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin heavy chain rearrangements.";
Bur. J. Immunol. 22:247-251(1992).
EMBL; AP035024; AA056260.1; -; mRNA.
PIR; S78486; 578486.
SNR; Q9UL90; 1-113.
                                                                                                                                                                                                                                                                                                                                      113 AA
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                                                                                                                                                                                                               20 BIQLVESGGGLVQPGGSLRLSCAAS 44
                                                                                                                                                                                                                                                                                                                                      PRT;
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InterPro, IPR003596; Ig-v.
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PROSITE; PS50835; IG LIKE; 1.
                                                                                             Query Match
Best Local Similarity 96.0%
                                                                                                                                                                                                                                                                                                                                    QUL90_HUMAN PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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21-JUL-1986
10-MAY-2005
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P01765;
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Q991190

HUM

DT 01-MA

DT 01-MA

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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
Hōmo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                   MEDLINES-78005528; PubMed=409716; Mang A.-C., Wang I.Y., Fudenberg H.H.; Mang A.-C., Wang I.Y., Pudenberg H.H.; Mang A.-C., Wang I.Y., Pudenberg H.H.; Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain."; J. Biol. Chem. 252:7192-7199(1977).

-i MSCRLIANROUS: The sequences of the V regions of the heavy chains of IgM and IgG2 isolated from a single patient with biclonal gammopathy are identical. Their light chains are apparently also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=74142702; PubMed=4522793; Capra J.D., Kehoe J.M.; Capra J.D., Kehoe J.M.; Capra J.D., Kehoe J.M.; Capra J.D., Kehoe J.M.; Warlable region sequences of five human immunoglobulin heavy chains of the VH3 subgroup; definitive identification of four heavy chain hypervariable regions.; Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
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SMR; P01765; 2-115.
GO; GO:0005276; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005855; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003566; Ig-v.
SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V-III region TUR.
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96.0%; Pred. No. ...
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P01776;
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SEQUENCE
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                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMES outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
13-SFS-2005 (Rel. 48, Last annocation update)
19 heavy chain V-III region VH26 precursor.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE OF 20-117.
MEDLINE=93209281; PubMed=7681398;
Mariette X., Tampis A., Brouet J.C.;
"Nucleotidic sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated glycoprotein.";
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-81101090; PubMed-6450418;
Matthyssens G., Rabbitts T.H.;
Structure and multiplicity of genes for the human immunoglobulin
heavy chain variable region." 77:6561-6565(1980).
SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                        97.6%; Score 120; DB 1; Length 116; 96.0%; Pred. No. 4.6e-09;
                                                                                                                                                                                                                                                             0; Indels
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                                                                             PIR; A02062; AlHUTU.

HSSP; P01783; 11GC.

GO; GO:0005576; C:extracellular region; NAS.

GO; GO:000823; F:antigen binding; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPRO07110; Ig-like.

InterPro; IPRO03596; Ig-v.

PROSITE; PSS0835; IG LIKE; I.

Direct protein sequencing; Immunoglobulin domain;

Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                          117 AA
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                                                                                                                                                                                                                                                             24; Conservative
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                                                                                                                                                                                                                                                   Best Local Similarity
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SEQUENCE
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HV3C HUMAN
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                           PIR; A02047; H3HU26.
PDB; 1HOU; Model; H=20-117.
PDB; C0:0003823; F:antigen binding; NAS.
POS: C0:0003823; F:antigen binding; NAS.
POS: C0:0003823; F:antigen binding; NAS.
PROSITE; PSG0835; IG LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
-!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
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PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
I 112
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V-III region WAS.
Homo sapiens (Human).
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GO; GO:0005576; C:extracellular region; NAS.

GO; GO:0003823; F:antigen binding; NAS.

GO; GO:0000555; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_V.
EMBL; J00236; AAAS3516.1; -; Unassigned DNA.
EMBL; M35415; AAAS8735.1; -; Genomic_DNA.
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21-JUL-1986 (Rel. 01, Last sequence update)
110-MAY-2005 (Rel. 47, Last annotation update)
110-MAY-2005 (Rel. 47, Last annotation update)
110-MAY-2005 (Rel. 47, Last annotation POM.
110-MAY-2005 (Human)
110-MAY-2015 (Human)
110-MAY-2015 (May Chordata; Craniata; Vertebrata; Euteleostomi;
110-MAMMANIA; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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N -> D (probably due to deamidation
during isolation).
/FTId=VAR_003966.
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                                 97.6%; Score 120; DB 1; Length 117; 96.0%; Pred. No. 4.7e-09; ive 1; Mismatches 0; Indels
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117 AA; 13091 MW; 201DBF0BIB53D9BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO: GO: 0005576; C: extracellular region; NAS. GO: GO: 0003823; F: antigen binding; NAS. GO; GO: 0003823; F: antigen binding; NAS. GO; GO: 0006955; F: immune response; NAS. InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM0406; IGv; 1.
PROSITE; PSS0835; IG-LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
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                                                                                                      1 EVQLLESGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                 PRT;
                                                               24; Conservative
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HSSP; P01772; 2FB4.
SMR; P01774; 1-119.
                                                 Best Local Similarity
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NCBI_TaxID=9606;
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Search completed: April 25, 2006, 06:24:39 Job time : 133.491 secs

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US-08-471-780C-80

Sequence 80. Application US/08471780C

Patent No. 575908

GENERAL INFORMATION:

APPLICANT: Casterman, Cecile

APPLICANT: Casterman, Cecile

APPLICANT: Casterman, Cecile

APPLICANT: Casterman, Cecile

APPLICANT: Casterman, Manuaglobulins Devoid of Light Chains

NUMBER OF SEQUENCES: 130

CORRESPONDENCE ADDRESS: 130

CORRESPONDENCE ADDRESS: 130

CONTYRY: Washington

STREET: 1300 I Street, N.W.

CITY: Washington

STREET: 1300 I Street, N.W.

CITY: Washington

STRATE: 1000-3315

COMPUTER REALABLE FORM:

MEDIUM TYPE: FILOPPY disk

COMPUTER REALABLE FORM:

MEDIUM TYPE: Compatible

OPPRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PREPICATION DATA:

APPLICATION NUMBER: US 08/106,944

FILING DATE: 1-AUG-1993

PRICE APPLICATION NUMBER: RF 92402326.0

FILING DATE: 21-AUG-1993

APPLICATION NUMBER: RF 93401310.3

FILING DATE: 1-AUG-1993

APPLICATION NUMBER: RF 93401310.3

FILING DATE: 1-AUG-1993

APPLICATION NUMBER: RF 93401310.3

FILING DATE: 1-AUG-1993

APPLICATION NUMBER: RF 93401310.3

FILING DATE: 21-AUG-1993

APPLICATION NUMBER: RF 93401310.3

FILING DATE: 1-AUG-1993

APPLICATION NUMBER: RF 93401310.3

FILING DATE: 21-AUG-1993

APPLICATION NUMBER: 33,332

RESERRENCE POCKET NUMBER: 83,332

RESERVENCE POCKET NUMBER: 93,933

APPLICATION NUMBER: 30,939

APPLICATION NUMBER: 30,939

FILING DATE: 21-AUG-1993

APPLICATION NUMBER: 30,939

APPLICATION NUMBER: 30,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
CRIGINAL SOURCE:
CREANISM: Camelus dromedarius
US-08-471-780C-80
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TYPE: amino acid
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                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-08-471-2828-80
US-08-466-710C-80
US-08-537-68A-80
US-08-537-87A-4
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US-08-211-202-116
US-08-212-245-37
US-08-65-202-31
US-09-315-574-31
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US-09-534-717-594

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US-09-534-717-595

US-09-534-717-596

US-09-899-896-9

US-09-899-896-9

US-08-428-197-4

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Sequence 80, Application US/08467282B

Patent No. 2800988

GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
ITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF ERQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
CITY: Washington
STATE: D.C.
CONTRY: USA
ZIP: 20005-3315
COMPUTER: EALOST N.W.

COMPUTER: ENDERS: Ploppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Dev.
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk:
COMPUTER: Ploppy
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Query Match 100.0%; Score 123; DB 1; Length 26; Best Local Similarity 100.0%; Pred. No. 2.2e-11; Matches 25; Conservative 0; Mismatches 0; Indels
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; Sequence 80, Application US/08471282A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REPERENCE/DOCKET NUMBER: 045
TELECOMMUNICATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-08-467-282B-80
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PAPLICANT: Casterman, Cecile
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
VORRESPONDENCES: 130
CORRESPONDENCES: 130
CORRESPONDENCES: 130
CITY: Washington Firmean, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington Street, N.W.
STREET: 1300 I Street, N.W.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER: IBM PC Compatible
COMPUTER: USA
SOFTWARE: PatentIn Release #1.0, Version #1.25
COMPATION TYPE: US/08/471,282A
FILING DATE: US-UN-1995
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 11FORMATION:
MANNEY AGENT: THOUGHAY-1993
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 11FORMATION:
MANNEY AGENT: THOUGHAY-1993
APPLICATION PATE: THOUGHAY-1993
APPLICATION PATE: THOUGHAY-1993
APPLICATION NUMBER: FR 93401310.3
APPLICATION NUMBER: FR 93401310.3
APPLICATION PATE: THOUGHAY-1993
APPLICATION PATE: THOUGHAY-19
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| Patent No. 5874541
| Patent No. 58745541
| Patent No. 58745541
| Patent No. 58746541
| Patent No. 58746541
| Patent No. 58746541
| Patent No. 587466710N: Cecile
| Patent Hamers, Raymond
| TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
| NUMBER OF SEQUENCES: 130
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Phinegan, Henderson, Farabow, Garrett & Dunner
| STREET: 1300 I Street, N.W. | CITY: Washington | STREET: USA | COUNTRY: USA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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100.0%; Score 123; DB 1;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Potter, Jane E.R. REGISTRATION NUMBER: 33,332 REPERENCE/DOCKET NUMBER: 045 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 80: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 amino acids
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005-3315
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US-08-466-710C-80
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; OTHER INFORMATION: Description of Unknown Organism: Camelus sp. ; OTHER INFORMATION: Lama sp. US-09-293-769A-80
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Sequence 80, Application US/09293769A;
Patent No. 6765087;
GENERAL INFORMATION:
APPLICANT: CASTERMAN, CECILE
APPLICANT: CASTERMAN, CECILE
TITLE OF INVENTION:
FILE REFERENCE: 04958.0008.07000
CURRENT APPLICATION NUMBER: US/09/293.769A;
FILE REFERENCE: 04958.0008.07000
CURRENT PILING DATE: 1999-04-19
FRIOR APPLICATION NUMBER: 08/471,284
FRIOR APPLICATION NUMBER: 08/471,284
FRIOR APPLICATION NUMBER: BPO 92402326.0
FRIOR PILING DATE: 1997-06-21
FRIOR PILING DATE: 1993-06-21
FRIOR FILING DATE: 1993-05-21
FRIOR FILING DATE: 1993-05-21
FRIOR FILING DATE: 1993-05-21
FRIOR FILING DATE: 1993-05-21
FRIOR PILING DATE: 1993-05-21
FRIOR FILING DATE: 1993-05-21
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Pred. No. 2.2e-11;
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                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REPRENCE/DOCKET NUMBER: 34,342
REPRENCE/CONTINION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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US-08-537-871A-4
; Sequence 4, Application US/08537871A
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein CRIGINAL SOURCE: protein CRGANISM: Camelus dromedarius US-08-468-739C-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                           TELEFAX: 202408-4400
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acide
21-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-293-769A-80
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,739C
FILING DATE: 06-7UN-1995
CLASSIPRICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
                                                                                                                                                                                                         PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-AUG-1993
APPLICATION NUMBER: FR 93401310.3
ATTORNEY-AGENT INFORMATION:
NAME: POCKET, Jane B.R.
REGISTRATION NUMBER: 33,332
REPRENCE/DOCKET NUMBER: 04958.0008-00000
TELEPONNICATION INFORMATION:
TELEPHONE: 202-408-400
TELEPHONE: 202-408-400
INFORMATION FOR SEG ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVESGGLVQPGGSLRLSCAAS 25
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-466-710C-80
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US-08-468-739C-80
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US-00-12-17

### Sequence 17, Application US/09855271

### Sequence 17, Application US/09855271

#### Sequence 17, Application US/09855271

#### Sequence 17, Application US/09855271

#### APPLICANT: Bodmer, Mark W

### APPLICANT: Athwal, Diljeet Singh

### APPLICANT: Athwal, Diljeet Singh

### APPLICANT: Batage, John Spencer

### TILE ON INVENTION: Interleukin-5 Specific Recombinant Antibodies

#### TILE ON INVENTION: Interleukin-5 Specific Recombinant Antibodies

### CURRENT APPLICATION NUMBER: US/09/855,271

### PRIOR PILING DATE: 1999-07-02

### NUMBER: O9/347,061

### NUMBER: O9/347,061

### SEQ ID NOS: 28

### SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09347061
Patent No. 631627
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Athwal, Diljeet Singh
APPLICANT: ARLage, John Spencer
TILLE REPERENCE: CARP-0071
CURRENT APPLICATION NUMBER: US/09/347,061
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 123; DB 2; Length 30;
Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                    Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                CLASSIPICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUJILLO, DORBER YATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: 37,719
REFERENCE/CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
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100.0%;
Best Local Similarity 100.0%;
Matches 25; Conservative 0.
06 JUNE-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc feature
; OTHER INFORMATION: Consensus
US-09-347-061-17
                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-470-139-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-347-061-17
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LENGTH: 30
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                                             APPLICANT: Raymond HAMERS
APPLICANT: Sergle HAMERS-CABSTERWAN
APPLICANT: Sergle V. M. MUYLDERMANS
APPLICANT: Leon G. J. FRENKER
APPLICANT: Cornelis T. VERRIPS
APPLICANT: Cornelis T. VERRIPS
TITLE OF INVENTION: Production of antibodies or (functionalized)
TITLE OF INVENTION: Craments thereof derived from heavy chain immunoglobulins
TITLE OF INVENTION: of Camelidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
TITLE OF INVENTION: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,139
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MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: human heavy chain framework (subgroup III)
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: Pillebury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDULUM TYPE: 1.44 Mb disk
COMPUTER: 118M PC COMPATIBLE
COMPUTER: 118M PC-DOS/MS-DOS
SOFTWARE: MICTOSOFT WORD
SOFTWARE: MICTOSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,871A
FILING DATE: 29-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/FP94/01442
FILING DATE: 28-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 93202079.5
FILING DATE: 19-MX-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 93201454.1
FILING DATE: 19-MX-1993
PRIOR APPLICATION DATA:
FILING DATE: 29-APR-1993
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE GHRACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acids
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Patent No. 5998586
GENERAL INFORMATION:
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Best Local Similarity 100.
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US-08-470-139-17
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RESULT 13
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100.0%; Score 123; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                 Query Match
100.0%; Score 123; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: FOOTE, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
FURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR PILIATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR PILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 97
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Patent No. 6881557
                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/10194975
Patent No. 6881557
                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                 ; OTHER INFORMATION: Consensus US-09-855-271-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-194-975-31
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US-10-194-975-31
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US-10-194-975-18
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LENGTH: 30
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Sequence 638, Application US/09534717

Patent No. 6914128
GENERAL INFORMATION:
APPLICANT: Jochen, Salfeld et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
TITLE OF INVENTION: WINBER: US/09/534,717
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 638
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MEDIUM TYPE: Floppy disk
COMPUTER: PORPY disk
COMPUTER: PLOPPY DISK
COMPUTER: PROPPY DISK
COMPUTER: PROPPY DISK
COMPUTER: PATENTING TO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNDBER: US/08/211,202
CLASSIFICATION DATA:
APPLICATION NUMBER: GB 912025.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: A-MAR-1992
PRIOR APPLICATION NUMBER: GB 9206372.6
PRIOR APPLICATION NUMBER: GB 9206372.6
PRIOR APPLICATION NUMBER: GB 9206372.6
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US-08-211-202-116

Sequence 116. Application US/08211202

Sequence 116. Application US/08211202

GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael
APPLICANT: WINTER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies:
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indela
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100.0%; Pred. No. 9.2e-11;
ive 0; Mismatches 0;
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APPLICATION NUMBER: PCT/GB92/00883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-638
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Best Local Similarity
Matches 25; Conserv
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100.0%; Score 123; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.3e-11;
Matches 25; Conservative 0; Mismatches 0; Indels
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Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: REES,
Anthony R.
APPLICANT: REES,
Anthony R.
APPLICANT: REES,
Anthony R.
APPLICANT: REES,
ATHONY R.
APPLICANT: GUILD,
APPLICANT: GUILD,
TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF INVENTION: ALLEGACE OF TRANSPORTED OF SEQUENCES: 522
CORRESPONDENCE ADDRESS: ADDRESSE: SUGHTUE, Mion, Zinn, Macpeak & Seas STRET: 2100 Pensylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUVERY: United States
ZIP: 20037-3202
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
COMPUTER: HP 9000/700 Workstation
OPERATION SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION UNIX
SOFTWARE: 10 HOUSE
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 6491103
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: peptide
FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: DAY16 W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
FILECOMMUNICATION INFORMATION:
FILEFPAN: 312-474-0448
FILEFRA: 25-3856
INFORMATION FOR SEQ ID NO: 116:
FELEX: 25-3856
INFORMATION FOR SEQ ID NO: 116:
FELUARY: 98 amino acids
FELUARY: 98 amino acids
FORDIOGY: Information acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-942-245-37
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1 EVQLVESGGGLVQPGGSLRLSCAAS 25

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1 EVQLVESGGGLVQPGGSLRLSCAAS
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Search completed: April 25, 2006, 06:28:40 Job time : 34.7264 secs

Sequence 7 Sequence 6 Sequence 7 Sequence 6

Sequence 7, A Sequence 6, A Sequence 37, Sequence 44, Sequence 90, Sequence 15, Sequence 18, Seq

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database :

Result Š

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Length 25;
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Publication No. US20040131612A1
GENERAL INFORMATION:
APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins, David
APPLICANT: Watkins, David
APPLICANT: Watkins, David
APPLICANT: Marquis, David
APPLICANT: Marguis, David
APPLICANT: Marguis, David
APPLICANT: Marguis, David
CURRENT HISTON TNF-alpha Binding Molecules
FILE REFERENCE: AME-0691
CURRENT PILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin version 3.2
SEQ ID NO 65
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-LIC-338-02/-05

J Sequence 55, Application US/10338627

Publication No. US20040131613A1

GENERAL INFORMATION

APPLICANT: Watkins, Jeffry D.

APPLICANT: Watkins, David

APPLICANT: Watkins, David

APPLICANT: Watkins, David

APPLICANT: Huse, William D.

TITLE OF INVENTION: TNF-alpha Binding Molecules

TITLE REFERENCE: AME-07497

CURRENT APPLICATION NUMBER: US/10/338,627

CURRENT FILING DATE: 2003-01-08

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.2

SEQ ID NO 65

LENGTH: 25

TYPE: PRT

CORGANISM: Homo sapiens

US-10-338-627-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 123; DB 4;
100.0%; Pred. No. 5.3e-10;
tive 0; Mismatches 0;
                      US-10-638-210-37
US-10-638-210-44
US-10-88-210-44
US-10-842-011-45
US-09-910-483-45
US-09-910-483-45
US-10-194-975-11
US-10-194-975-13
US-10-194-975-13
US-10-103-0378-69
US-10-032-0378-69
US-10-032-9888-78
US-10-032-9888-78
US-10-032-9888-78
US-10-032-9888-78
US-10-032-9888-78
US-10-032-9888-78
                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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ORGANISM: Homo sapiens
US-10-338-552-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 25; Conserv
RESULT 2
US-10-338-627-65
                                                                                                                                                                                                                                                                                                                                                                    US-10-338-552-65
TYPE: PRT
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Sequence 321, App
Sequence 339, App
Sequence 363, App
Sequence 366, App
Sequence 372, App
Sequence 372, App
Sequence 4, Appl
Sequence 17, Appl
Sequence 121, Appl
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Sequence 65, Appl
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                                                                                                       April 25, 2006, 06:58:17 ; Search time 108.962 Seconds (without alignments) 95.866 Million cell updates/sec
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Sequence 2
Sequence 2
Sequence 2
Sequence 1
Sequence 3
Sequence 3
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA Main: * /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-758-04.7 e3

US-10-923-068-315

US-10-923-068-321

US-10-923-068-348

US-10-923-068-348

US-10-923-068-36

US-10-923-068-36

US-10-923-068-375

US-10-923-068-375

US-10-915-490-4

US-10-915-490-4

US-10-915-490-4

US-10-915-491

US-10-913-068-106

US-10-923-068-106

US-10-923-068-106

US-10-923-068-207

US-10-923-068-216

US-10-923-068-216
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                                                                                                                                                                                                                                                                              1867569 seqs, 417829326 residues
                                                                                                                                                                     US-10-764-428-3
123
1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Gaps

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RESULT 6
US-10-923-068-339
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                                                                                                                                                                                                                                 Sequence 3, Application US/10764428
Publication No. US20040229310A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
TITLE OF INVENTION: TIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
TITLE OF INVENTION: CULTURE
FILE REFERENCE: 11669.1200301
CURRENT APPLICATION NUMBER: US/10/764,428
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,484
PRIOR PILING DATE: 2003-01-23
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      Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 25;
                                                 0; Indels
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100.0%; Score 123; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0;
    ch 100.0%; Score 123; DB 4;
1. Similarity 100.0%; Pred. No. 5.3e-10;
25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-10-923-068-315
; Sequence 315, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
; APPLICANT: Wu, Herren
; APPLICANT: Dall'Acqua, William
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
; FILE REFERENCE: AE600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SSOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                  1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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                                                                                           1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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SOFWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 25
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; ORGANISM: Homo sapiens
US-10-923-068-315
Query Match
Best Local Similarity
Matches 25; Conserva
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Sequence 321, Application US/10923068
Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Dall'Acqua, William
APPLICANT: Damschroder, Melissa
ITILE OF INVENTION: HUMANIZATION OF ANTIBODIES
CURRENT APPLICANTION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 321
LENGTH: 25
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Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Damschroder, Melissa
APPLICANT: Damschroder, Melissa
APPLICANT: PLICATION UNMBER: US/10/923,068
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT PILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SEQ ID NOS: 518
LENGTH: 25
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Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Danschroder, Melissan
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
TILL REFRENCE: AE60US
CURRENT PLING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
LIENGTH: 25
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CORGANISM: Homo sapiens
US-10-923-068-321
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CORGANISM: Homo sapiens
US-10-923-068-339
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TYPE: PRT
CORGANISM: Homo sapiens
US-10-923-068-372
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US-10-751-826-80
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US-10-915-490-4
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Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                       Length 25;
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100.0%; Score 123; DB 5; Length 2
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                           Indels
                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                    Sequence 363, Application US/10923068

Publication No. US20050042664A1

GENERAL INFORMATION:
APPLICANT: Wu, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Damchroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT PILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 363
LENGTH: 25
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Publication No. US200500426641

GENERAL INFORMATION:

APPLICANT: Wu, Herren
APPLICANT: Damschroder, Melissa

TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES

TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES

CURRENT APPLICATION NUMBER: US/10/923,068

CURRENT PILING DATE: 2004-08-20

NUMBER OF SEQ ID NOS: 518

SOFTWARE: FestSEQ for Windows Version 4.0

SEQ ID NO 366

LENGTH: 25
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                                                                                                                                                1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-10-923-068-366
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CORGANISM: Homo sapiens
US-10-923-068-363
     ; TIPE: FAI
; ORGANISM: Homo sapiens
US-10-923-068-348
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US-10-923-068-363
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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APPLICANT: CASTERWAN, CECTIE
APPLICANT: CASTERWAN, CECTIE
APPLICANT: HAMERS, RAYMOND
TITLE OF INVENTION: INMUNOCLOBULINS DEVOID OF LIGHT CHAINS
FILE REFERENCE: 0.958, 0.008-0.7000
CURRENT FILING DATE: 1.090-0.4-19
PRIOR APPLICATION NUMBER: 0.8/10/751,826
PRIOR APPLICATION NUMBER: 0.8/471,284
PRIOR PILING DATE: 1.999-0.4-19
PRIOR PILING DATE: 1.999-0.6-06
PRIOR PILING DATE: 1.999-0.6-06
PRIOR PILING DATE: 1.997-0.1-15
PRIOR PAPLICATION NUMBER: EPO 92402326.0
PRIOR PILING DATE: 1.993-0.6-11
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100.0%; Score 123; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.5e-10;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e-10;
Matches 25; Conservative 0; Mismatches 0;
Sequence 372, Application US/10923068
Publication No. US20050042664A1
GENERAL INFORMATION:
APPLICANT: William
APPLICANT: Dail'Acqua, William
APPLICANT: Dail'Acqua, William
APPLICANT: DameNroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
CURRENT FILING DATE: 2004-08-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: PateSEQ for Windows Version 4.0
SEQ ID NO 372
LENGTH: 25
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Publication No. US20050130266Al
GENERAL INFORMATION:
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RESULT 10 US-10-923-068-372 ö

Gaps

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Query Match 100.0%; Score 123; DB 3; Length 30; Best Local Similarity 100.0%; Pred. No. 6.4e-10; Matches 25; Conservative 0; Mismatches 0; Indels
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US-09-949-559-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 123; DB 3; 100.0%; Pred. No. 6.4e-10;
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APPLICANT: Brown, Derek Thomas
APPLICANT: Brown, Derek Thomas
APPLICANT: Brown, Derek Thomas
APPLICANT: Chapman, Andrew George
APPLICANT: Chapman, Andrew Paul
APPLICANT: King, David John
TILE OF INVENTION: Biological Products
FILE REFERENCE: Carp-0089
CURRENT APPLICATION NUMBER: US/09/875,221A
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR APPLICATION NUMBER: GB0013810.7
PRIOR STOIN NOS: 130
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVOLVESGGGLVQPGGSLRLSCAAS
                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                         FEATURE:
COTHER INFORMATION: Consensus
US-09-855-271-17
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Best Local Similarity
Matches 25; Conserva
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LENGTH: 30
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                                                                             Cornelis T. VERRIPS
TITLE OF INVENTION: Production of antibodies or (functionalized)
fragments thereof derived from heavy chain immunoglobulins
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Sequence 17, Application US/09855271

Fatent No. US2002004208941

GENERAL INFORMATION:

APPLICANT: Bodmer, Mark W

APPLICANT: Berage, John Spencer

TITLE OF INVENTIOR Interleukin-5 Specific Recombinant Antibodies

FILE REFERENCE: CARP-0088

CURRENT APPLICATION NUMBER: US/09/855,271

CURRENT APPLICATION NUMBER: 2001-05-15

PRIOR PILING DATE: 1999-07-02

FRIOR PILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: human heavy chain framework (subgroup III) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                 ADDRESSEE: Pillabury Madison & Sutro, L.L.P. STREET: 1100 New York Avenue, N.W. CITY: D.C.
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: 1BM FC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/915,490
FILING DATE: 11-Aug-2004
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/537,871
FILING DATE: 29-JAN-1996
APPLICATION NUMBER: FCT/EP94/01442
FILING DATE: 29-JAN-1996
APPLICATION NUMBER: PCT/EP94/01442
FILING DATE: 19-APR-1994
APPLICATION NUMBER: EPO 93201454.1
FILING DATE: 19-MAY-1993
APPLICATION NUMBER: EPO 93201239.6
FILING DATE: 29-APR-1993
APPLICATION NUMBER: EPO 93201239.6
FILING DATE: 29-APR-1993
                    Cecile HAMERS-CASETERMAN
Serge V. M. MUYLDERMANS
Leon G. J. FRENKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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                                                                                                                                                     of Camelidae
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TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
APPLICANT: Raymond HAMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                       NUMBER OF SEQUENCES: 7. CORRESPONDENCE ADDRESS
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Best Local Similarity 100.
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                 COUNTRY: USA
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US-09-855-271-17
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Length 30; Indels

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                                                                                                                              Query Match 100.0%; Score 123; DB 3; Length 30; Best Local Similarity 100.0%; Pred. No. 6.4e-10; Matches 25; Conservative 0; Mismatches 0; Indels
; SEQ ID NO 121
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 3 consensus framework H1
US-09-875-221A-121
                                                                                                                                                                                                      1 EVQLVESGGGLVQPGGSLRLSCAAS 25
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Search completed: April 25, 2006, 07:08:48 Job time : 109.962 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                     April 25, 2006, 07:01:21; Search time 16.0377 Seconds (without alignments) 68.593 Million cell updates/sec
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1. /SIDSS/ptodata/1/pubpaa/US06 NEW FUB.pep:*

2. /SIDSS/ptodata/1/pubpaa/US06 NEW FUB.pep:*

3. /SIDSS/ptodata/1/pubpaa/US07 NEW FUB.pep:*

4. /SIDSS/ptodata/1/pubpaa/PCT_NEW FUB.pep:*

5. /SIDSS/ptodata/1/pubpaa/US09 NEW FUB.pep:*

7. /SIDSS/ptodata/1/pubpaa/US10 NEW FUB.pep:*

7. /SIDSS/ptodata/1/pubpaa/US11 NEW FUB.pep:*

8. /SIDSS/ptodata/1/pubpaa/US11 NEW FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                              US-10-764-428-3
123
1 BVQLVBSGGGLVQPGGSLRLSCAAS 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          225428 seqs, 44002918 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                     Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
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Appl Appl Appl	Appl Appl	Appl Appl Appl	Appl Appl Appl Appl	Appi Appi Appi Appi Appi
36, 39,	47,	68, 68,	73.73	75, 77, 78, 79,
Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence
US-11-136-250-36 US-11-136-250-39 US-11-136-250-44	US-11-136-250-47 US-11-054-669-32 US-11-084-554-45	US-11-004-590-35 US-11-136-250-45 US-11-155-843-58 US-11-155-843-68	US-11-155-843-70 US-11-155-843-71 US-11-155-843-72 US-11-155-843-74	US-11-155-843-75 US-11-155-843-76 US-11-155-843-77 US-11-155-843-79
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## ALIGNMENTS

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CHERENT LAZAR, GREGOTY Alan
APPLICANT: LAZAR, GREGOTY Alan
APPLICANT: LAZAR, GREGOTY ALAN
APPLICANT: Desjarlais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: METHODS OF GREEKATING VARIANT PROTEINS WITH INCREASED HOST STRING
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
FILE REFERENCE: 155832/US/5
CURRENT APPLICATION NUMBER: US 60/527,167
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR PILING DATE: 2004-06-21
PRIOR PILING DATE: 2004-06-21
PRIOR PILING DATE: 2004-06-11
PRIOR PILING DATE: 2004-06-11
PRIOR PILING DATE: 2004-06-13
PRIOR PILING DATE: 2004-06-13
PRIOR PILING DATE: 2004-06-13
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PRIOR PILING DATE: 2004-06-13
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Publication No. US20060024296A1
GENERAL INFORMATION:
APPLICATION THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
FILE REPERENCE: file
CURRENT APPLICATION NUMBER: US/10/982,357
CURRENT FILING DATE: 2004-11-05
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US-11-004-590-113
; Sequence 113, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.3
SEQ ID NO 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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US-10-982-357-39
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RESULT 7
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                                                                                                                                                                  Length 44;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46, Application US/10982357
Publication No. US2006002429641
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/982,357
CURRENT PILING DATE: 204-11-05
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                       Indels
                                                                                                                                                                Query Match 100.0%; Score 123; DB 6; Best Local Similarity 100.0%; Pred. No. 6.8e-10; Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/11054669; Publication No. US20050261480A1; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES; FILE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669; CURRENT FILING DATE: 2005-02-08; PRIOR APPLICATION NUMBER: US 10/194,975; PRIOR APPLICATION NUMBER: US 60/305,111; PRIOR APPLICATION NUMBER: US 60/305,111; PRIOR FILING DATE: 2001-07-12; NUMBER OF SEQ ID NOS: 124; SEQ ID NO 18; SEQ ID NO 18
                                                                                                                                                                                                                                               1 EVQLVESGGLVQPGGSLRLSCAAS 25
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NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin version 3.2
SEQ ID NO 39
LENGTH: 44
                                                                               TYPE: PRT; ORGANISM: Homo sapiens
US-10-982-357-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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| Bublication No. US20050260679A1
| GENERAL INPORMATION:
| GENERAL INPORMATION:
| APPLICANT: Kellermann, Sirid-Ai
| APPLICANT: Green, Larry L.
| APPLICANT: Korver, Wouter
| TILLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
| TITLE OF INVENTION: AMTIBODIES THROUGH V GENE MANIPULATION
| TILLE OF INVENTION: AUTIBODIES THROUGH V GENE MANIPULATION
| TILLE OF INVENTION: AUTIBODIES THROUGH V GENE MANIPULATION
| TILLE OF INVENTION: UNMERR: 100/11/084,554
| CURRENT PAPLICATION NUMBER: 60/554,372
| PRIOR FILING DATE: 2004-03-19
| PRIOR PILING DATE: 2004-03-19
| PRIOR PILING DATE: 2004-03-19
| PRIOR PILING DATE: 2004-05-24
| NUMBER OF SEQ ID NOS: 266
| SOFTWARE FREIES FREICE FOR Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0;
                                                                            TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/UG.
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
SROFTWARE: Patentin version 3.3
SEQ ID NO 31
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Sequence 31, Application US/11054669 Publication No. US20050261480A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/11004590; Publication No. US20060008883A1; GENERAL INFORMATION:
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US-11-054-669-31
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                             GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Genen, Larry L.

APPLICANT: Green, Larry L.

APPLICANT: Green, Larry L.

APPLICANT: Green, Larry L.

APPLICANT: Green, Larry L.

TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION

FILE REPERENCE: AGGRNIX.1002

CURRENT APPLICATION NUMBER: US/11/136,250

CURRENT FILING DATE: 2005-03-17

PRIOR APPLICATION NUMBER: ECT/US2005/009306

PRIOR PILING DATE: 2005-03-17

PRIOR FILING DATE: 2005-03-17

PRIOR FILING DATE: 2005-03-17

PRIOR FILING DATE: 2004-03-19

PRIOR FILING DATE: 2004-03-19

PRIOR FILING DATE: 2004-03-19

PRIOR FILING DATE: 2004-03-19

NUMBER OF SEQ ID NOS: 266

SOFTWARE: PARESEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 123; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0;
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FILE REFERENCE: 30219/US,
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT PILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR PILING DATE: 2002-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-12
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.3
SEQ ID NO 15
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19-11-054-669-28
19-11-054-669-38
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    Publication No. US20060021074A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-11-136-250-28
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CORGANISM: Homo sapiens
US-11-054-669-15
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| Bequence 34 Application US/11004590
| Publication No. US20060008883A1
| GENERAL INFORMATION:
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Lazar, Gregory Alan
| APPLICANT: Hammond, Phillip W. |
| TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING TITLE OF INVENTION: METHODS OF GENERATING STRING STRING STRING DATE: 2004-12-03
| PRIOR PPLICATION NUMBER: US 60/527,167
| PRIOR PLING DATE: 2004-06-21
| PRIOR PLING DATE: 2004-10-14
| NUMBER OF SEQ ID NOS: 458
| SOFTWARE: Patentin version 3.3
| SEQ ID NO 34
| LENGTH: 97
APPLICANT: Desjarlais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
CURRENT APPLICATION NUMBER: US 60/527,167
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR PILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/601,665
PRIOR FILING DATE: 2004-06-21
PRIOR PILING DATE: 2004-10-14
PRIOR FILING DATE: 2004-10-14
NUMBER OF SEQ ID NOS: 458
SSO ID NOS: 458
SSO ID NO 17
LENGTH: 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 123; DB 7; Length 97; Best Local Similarity 100.0%; Pred. No. 1.4e-09; Matches 25; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0;
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; Sequence 28, Application US/11136250
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US-11-004-590-34
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US-11-004-590-17
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Sequence 36, Application US/11084554
; Publication No. US20050260579A1
; General information:
GENERAL INFORMATION:
APPLICANT: Kellermann, Sirid-Ai
APPLICANT: Green, Larry L.
FAPLICANT: Green, Larry L.
TILLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
FILE REPRENENCE ABGENIX.100A
CURRENT FILING DATE: 2005-03-17
PRIOR PILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR FILING DATE: 2004-03-19
PRIOR FILING DATE: 2004-05-24
; WUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-084-554-30

| Sequence 30, Application US/11084554
| Publication NO. US2055026679A1
| GENERAL INFORATION:
| APPLICANT: Kellermann, Sirid-Ai
| APPLICANT: Green, Larry L. Green, Larry L. BOTTLER OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION TITLE OF INVENT APPLICATION NUMBER: US/11/084,554
| CURRENT FILING DATE: 2005-03-17
| PRIOR FILING DATE: 2004-03-17
| PRIOR FILING DATE: 2004-05-24
| NUMBER OF SEQ ID NOS: 266
| SOFTWARE: FREUER Windows Version 4.0
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Best Local Similarity 100.0%; Score 123; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0: Indela
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                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                 Conservative
                                             ; ORGANISM: Homo sapiens
US-11-054-669-33
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ORGANISM: Homo sapiens
US-11-084-554-30
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Best Local Similarity
Matches 25; Conserv
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100.0%; Score 123; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 25; Conservative 0; Mismatches 0;
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Publication No. US20050261480A1
GENERAL INFORMATION:
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Publication No. US20050261480A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3
CURRENT FILING DATE: 2005-02-08

PRIOR APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-07-12
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR PILING DATE: 2001-07-12

PRIOR FILING DATE: 2001-07-12

NUMBER OF SEQ ID NOS: 124

SOFTWARE: PALENT VERSION 3.3

LENGTH: 98
FILE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
FRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR PILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
LENGTH: 98
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ORGANISM: Homo sapiens
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US-11-054-669-30
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Matches 25
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Gaps ö Best Local Similarity 100.0%; Pred. No. 1.4e-09; Matches 25; Conservative 0; Mismatches 0; Indels

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Search completed: April 25, 2006, 07:10:01 Job time : 16.2044 secs

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- protein search, using sw model OM protein Run on:

April 25, 2006, 06:15:41; Search time 8.49057 Seconds (without alignments) 113.322 Million cell updates/sec

US-10-764-428-14 58 Title: Perfect score: Sequence:

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Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

PIR 80: * 1: piri: * 2: pir2: * 3: pir3: * 4: pir4: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Ig heavy chain V	heavy chain V	heavy chain V	heavy	heavy chain V	heavy	heavy	_	heavy	heavy chain	heavy chain V	mAb heavy chai	heavy chain	heavy	heavy chain	heavy chain V	heavy chain	heavy chain V	heavy chain V	heavy chain V	heavy	heavy chain V	heavy chain	Ig heavy chain V r					
QI	A36194	C24672	826326	D24672	S24764	S24765	S26325	S19968	819965	S19967	A53285	B42848	PH1404	833905	B28572	B24754	A28572	PH1491	PH1490	PH1523	PH1522	838565	A24754	PH1510	PH1505	PH1518	PH1517	PH1502	PH1500
80	~	~	~	~	~	~	~	~	~	~	~	~	~	4	~	~	~	~	~	~	~	N	N	ď	~	~	~	~	0
Vuery Match Length DB	140	93	66	101	105	105	109	115	115	118	119	120	124	146	16	96	98	102			114	118			119	119	119	119	119
Match	100.0	•		•	•	•		94.8	•		•	•	•	•	91.4	91.4		91.4		91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4
Score	58	55	55	55	55	55	55	55	55	55	55	55	55	55	53	53	53	53	53	53	53	53	53	53	53	53	53	53	23
Regult No.	-	7	m	4	'n	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

	Ig heavy chain V-D Ig heavy chain V r Ig heavy chain V r
PH1503 PH1504 PPH1504 A21854 A21854 A21854 PH1492 PH1492 PH1492 PH1483 PH1482 A32189 G48677	E48677 PH1493 PH0988
0000000000000	000
1119 1119 1121 1121 1135 1140 1140 1123	123 135 111
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	89.7 89.7 87.9
22223333333333333333333333333333333333	52 51 51
	4 4 4 6 4 3

### ALIGNMENTS

RESULT 1 A36194

Gapa ö 100.0%; Score 58; DB 2; Length 140; 100.0%; Pred. No. 0.005; varive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 10; Conservative

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1 GYTFTNYGIN 10 

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RESULT 2

January chain V region (VMU-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C;Date: 12467, 1988
R;Minter, B.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Residues: 1-93 < WINA
C;UPIO000113757; GB:X03300; NID:952375; PIDN:CAA27039.1; PID:9
C;Reywords: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin

Gaps ö Query Match

94.8%; Score 55; DB 2; Length 93;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels

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1 GYTFTNYGIN 10

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A,Residues: 1-105 <THO>
A,Cross-references: UNIPARC:UPI000011648C; EMBL:215020; NID:952616; PIDN:CAA78739.1; PID
C,Genetics:
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R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein eg
A;Reference number: S26309; MUID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPROT: Q921A6; UNIPARC: UPI000017696F; EMBL: X59210; NID: 952080; PID: g
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C;Species: Wus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence revision 21-Nov-1998 #text_change 23-Jul-1999
C;Accession: $24765; $24773; $24778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                       Length 105;
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C;Keywords: heterotetramer; immunoglobulin
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A;Molectule type: DNA
A;Residues: 1-105 < KIA>
A;Cross-references: UNIPARC:UPI000011648E; EMBL:Z15001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: UNIPARC: UPI000011648B; EMBL: 215013
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Pred. No. 0.013;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   94.8%; Score 55; DB 2;
90.0%; Pred. No. 0.013;
tive 1; Mismatches
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submitted to the EMBL Data Library, August 1992
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submitted to the EMBL Data Library, August 1992
A;Reference number: S24776
AAccession: S24778
submitted to the EMBL Data Library, August 1992
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Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYTFTNYGIN 10
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                              A, Reference number: S24776
A, Accession: S24777
A, Molecule type: DNA
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A; Residues: 1-105 < KLW>
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A; Residues: 1-105 <THO>
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A,Residues: 1-109 <STA>
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A;Status: preliminary
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Best Local S:
Matches 9,
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Jigheavy chain V region (VGAM3-8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C;Accession: D24672
R;Winter, Es; Radburch, A.; Krawinkel, U.
R;Winter, Es; Radburch, A.; Krawinkel, U.
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Reference number: D102; MUID:86055722; PMID:2998759
A;Reference number: Jul < WIN>
A;Reference number: Jul < WIN>
A;Residues: 1-101 < WIN>
A;Residues: 1-101 < WIN>
A;Residues: UNIPARC:UPIO000113758, GB:X03301; NID:951757; PIDN:CAA27040.1; PID:9
A;Notes: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                            Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C;Accession: S26326
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Fitle: Antibodies that are specific for a single amino acid interchange in a protein A;Reference number: S26309; MUID:91341421; PMID:1908510
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C;Species: Mus musculus (house mouse)
C;Accession: S24764; S24772; S24777
R;Klages, S.
Submitted to the EMBL Data Library, August 1992
A;Reference number: S24764
A;Reference number: S24764
A;Molecule type: DNA
A;References: UNIPARC:UPI000011648C; EMBL:Z14999
A;Cross-references: UNIPARC:UPI000011648C; EMBL:Z14999
A;Accession: S24772
A;Molecule type: DNA
A;Consolecule type
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A;Residues: 1-99 <STA>,
A;Croselsereferences: UNIPARC:UPI00001769AC; EMBL:X59174
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.8%; Score 55; DB 2; Length 101; 90.0%; Pred. No. 0.012; tive 1; Mismatches 0; Indels
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A;Cross-references: UNIPARC:UPI000011648C; EMBL:Z15011
R;Thomas, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 2;
Pred. No. 0.012;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Query Match Best Loca Matches

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519965
Ig heavy chain V region (M-T321) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 06-Peb-1995 #sequence_revision 06-Peb-1995 #text_change 31-Dec-2004
C; Accession: 319965
R; Weissenhorn, W: Riethmueller, G.; Weiss, E.W.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A; Pescription: Structural characterization of CD4 mab.
A; Reference number: $19963
A; Accession: $19965
A; Status: preliminary
A; Molecule type: mENA
A; Residues: 1-115 < WEI>
A; Cross-references: UNIPROT:0921A6; UNIPARC:UPI0000176968; EMBL:X65088
C; Reywords: heterotetramer; immunoglobulin
C; Reywords: heterotetramer; immunoglobulin homology < IMM>
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                                                                                                                                      Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 115
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                                                                                                                                          Score 55; DB 2;
Pred. No. 0.013;
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                                                                                                                                                                                                             1; Mismatches
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;S-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                             94.8%;
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                                                                                                                                                                           Local Similarity 90.0
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Matches 9; Conserv
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hes 9; Conserv
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S19967 Ig heavy chain V region (M-T406) - mouse (fragment) C;Species: Mus musculus (house mouse)

RESULT 10

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Risawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 103-1072, 1991
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary strucand their pH-reactivity profiles.
A;Reference number: A53285; MUID:92017897; PMID:1922102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA; protein
A; Molecule type: DNA; protein
A; Mesidues: 1-19 cSAN-
A; Cross-references: UNIPARC: UPIO00011D0A7; GB: D12736; NID: g220595; PIDN: BAA02228.1; PID: A; Cross-references: UNIPARC: UPIO00011D0A7; GB: D12736; NID: g220595; PIDN: BAA02228.1; PID: A; Note: sequence extracted from NCBI backbone (NCBIN: 63271, NCBIP: 63299)
A; Note: sequence extracted from NCBI backbone (NCBIN: 63271, NCBIP: 63299)
C; Superfamily: immunoglobulin immunoglobulin homology < IMM>
F; 15-98/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Caccession: A:Ascession: A:Ascession - mouse - mo
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A;Molecule type: DNA
A;Molecule type: DO 4FEL>
A;Cross-references: UNIPARC:UPI0000115333; GB:M90690; NID:g195065; PIDN:AAA38146.1; PID:
A;Note: sequence extracted from NCBI backbone (NCBIN:109960, NCBIP:109961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V and J regions, monoclonal antibody SCET.MB.1 - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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06-Feb-1995 #sequence_revision 06-Peb-1995 #text_change 31-Dec-2004
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                                                        C;Accession: S19967
R;Weissenhorn, W.; Rtethmueller, G.; Weiss, E.M.; Rieber, E.P.
R;Weissenhorn, W.; Rtethmueller, G.; Weiss, E.M.; Rieber, E.P.
R;Weissenhorn, W.; Rtethmueller, G.; Warch 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Reference number: S19963
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <WEI>
A;Cessences: UNIPROT: Q921A6; UNIPARC: UPI0000176969; EMBL: X65090
C;Superfamily: immunoglobulin homology
C;Superfamily: immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.014;
1; Mismatches
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Pred. No. 0.014;
1; Mismatches
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Best Local Similarity 90.v-
9, Conservative
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Search completed: April 25, 2006, 06:26:11
Job time : 9.49057 secs
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                                                                                                                                                                                                                                                                                                                                                             PH1404

Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

Ig heavy chain V region (clone micro m+ 46-12) - mouse (fragment)

C;Specdes: Mus musculus (house mouse)

C;Decdes: Muscalus (house mouse)

C;Accession: PH1404; PH1406

C;Accession: PH1404; PH1406

R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta J. Exp. Med. 176, 1209-1214, 1992

M;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S33905
Ig heavy chain precursor V region - synthetic
C;Species: synthetic
C;Species: synthetic
C;Species: 13-3na-1995 #sequence_revision 30-Apr-1998 #text_change 20-Oct-2000
C;Accession: 333905
C;Accession: 8.33905
C;Accession: S33905
C;Accession: S33905
A;Title: Chimeric mouse-human Igd1 antibody that can mediate lysis of cancer cells.
A;Reference number: S33905; MUD:87204152; PMID:3106970
A;Accession: S33905
A;Accession: BMAA38229.1; PI
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A;Cross-references: UNIPARC:UPI0000115333; EMBL:M90691
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;IS-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-118/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.8%; Score 55; DB 2; Length 124; ilarity 90.0%; Pred. No. 0.015; Conservative 1; Mismatches 0; Indels
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Pred. No. 0.018;
1; Mismatches 0; Indels
                                                                                                     Length 120;
                                                                                                                                                             0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: PH1403; MUID: 93018837; PMID: 1402663
                                                                                                       Score 55; DB 2;
Pred. No. 0.014;
                                                                                                                                                          1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-124 <SHI>
A;Cross-references: UNIPARC:UP1000017694C
A;Accession: PH1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Reaidues: 115-121 <SH2>
A;Cross-references: UNIPARC:UP1000017694C
                                                                                                          94.8%;
90.0%;
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Matches 9; Conservative
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Matches 9; Conserv
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RESULT 15

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A; Molecule type: DNA
A; Residues: 1-76 cSIEs
A; Residues: 1-76 cSIEs
A; Cross-references: UNIPARC:UPI0000114908; GB:K02154; GB:M17032; NID:g196176; PIDN:AAA380
A; Note: this sequence was determined from the germline gene
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                C;Accession: B28572
R;Siekevitz, M.; Huang, S.Y.; Gefter, M.L.
Bir. J. Immunol. 13, 123-132, 1983
A;Title: The genetic basis of antibody production: a single heavy chain variable region A;Reference number: A91262; MUID:83157801; PMID:6403356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Ig heavy chain V regions (CR-Id 7, CR-Id 14) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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91.4%; Score 53; DB 2; Length 76;
Best Local Similarity 90.0%; Pred. No. 0.021;
Matches 9; Conservative 1; Mismatches 0; Indels
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 25, 2006, 06:05:44 ; Search time 53.3962 Seconds (without alignments) 132.131 Million cell updates/sec Run on:

US-10-764-428-14 58 1 GYTFTNYGIN 10 Title: Perfect score: Sequence:

Scoring table:

2166443 segs, 705528306 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

**Database**:

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARTES

		40			SUMMAKIES	
Result No. 1	Score	Query Match	Length	DB		Description
-	53	91.4	120	-	HV03_MOUSE	mu8
7	23	91.4		ч	HV02_MOUSE	Enm
9	20	86.2		~	Q921A6_MOUSE	_
4	20	86.2	475	7	QSPQS1_RAT	ratt
'n	47	81.0	486	N	QSHZY6 MOUSE	e mus
9	46	79.3	117	ч	HV52_MOUSE	_
7	46	79.3	458	~	QSBJZ2_RAT	ratt
8	46	79.3	463	~	Q99LC4_MOUSE	ม ยกม เ
6	45	77.6	125	~		homo sap
10	45	77.6	140	~	Q65ZL3_9MURI	_
11	45	77.6	233	~	Q4ZGV0 9BACT	0 unid
12	44	75.9	121	-	HV01 MOUSE	mus
13	44	75.9		~	Q569W9_MOUSE	enm 6
14	44	75.9	473	7	Q9D8L4 MOUSE	mus
15	44	75.9		N	Q4V9V8_MOUSE	
16	43	74.1		•	Q6X2N8_9BACT	
17	43	74.1		•	Q6X2P6_9BACT	-
18	43	74.1	220	•	Q6X2P9_9BACT	_
19	43	74.1		•	QBRT26 9BACT	-
20	43	74.1	220	7	Q9AP60 9BACT	-
21	43	74.1			Q9AP61_9BACT	-
22	43	74.1	220	•	Q9AP62_9BACT	
23	43	74.1	220	N	Q9AP63 9BACT	
24	43	74.1	220		Q6X2Q0_9BACT	
25	43	74.1	220		Q6X2P0 9BACT	-
26	43	74.1	220	~	Q6X2N9 9BACT	-
27	43	74.1	233		Q4ZGQ6_9BACT	
28	43	74.1	233		Q4ZGQ7_9BACT	
29	43	74.1	233		Q4ZGR1_9BACT	
30	43	74.1	233	~	Q4ZGR9_9BACT	
31	43	74.1	233	7	Q4ZGS0_9BACT	Q4zgs0 unidentifie

04zgs4 unidentifie 04zgt7 unidentifie 04zgt3 unidentifie 05cjal cryptospori 05cjal cryptospori 05cjal cryptospori 05cjal cryptospori 05cjal cryptospori 05cjal cryptospori 06czk4 cryptospori 06czk4 cryptospori 06czk4 cryptospori 06czgł uncultured 06czgł uncultured 06czgł uncultured 06czgł uncultured 05cłgl uncultured 05cłgl uncultured 05cłgl uncultured
042GS4 9BACT 04ZGT7_9BACT 05ZGT3_9BACT 05CJA1_CRYHO 05CJA1_CRYHO 05CXA4_CRYPV HVS9 MOUSE HV35 MOUSE HV35 HUWAN 06CZP4_9BACT 06XZP4_9BACT 06XZP4_9BACT 06XZP4_9BACT 05D3G1_9BACT 05D3G1_9BACT
<b>0000000000000000000000000000000000000</b>
2333 2333 2233 2220 2220 2224 2244 2244
44444777777777777777777777777777777777
W W W W W W W W W W W W W W W W W W W
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

# ALIGNMENTS

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Muridae, Murinae, Mus
                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Igha protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Igha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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QSPQS1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J00493; AAA38128.1; -; mRNA.
HSSP; P01747; LJFQ.
SMR; P01746; 20-140.
InterPro; IPR00310; Ig-like.
InterPro; IPR003596; Ig-v.
SMRAT; SMRO406; IGV;
PROSITE; PSS0815; IG LIKE; 1.
PROSITE; PSS0815; IG LIKE; 1.
Hybridome; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.4%; Score 53; DB 1; Length 140; 90.0%; Pred. No. 0.18;
                    DB 1; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region 93G7. Ig-like.
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                                                        0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-CEA 79 single chain Fv (Fragment).
                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AA.
                                                                                                                                                                                                                                  140 AA.
                Score 53; DB 1; Pred. No. 0.15; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                    91.4%;
90.0%;
Query Match
Best Local Similarity 90.05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q921A6 MOUSE PRELIMINARY;
Q921A6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                    STANDARD;
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                                                                                                 GYTPTNYGIN 10
                                                                                                                     GYTETSYGIN 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE
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les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                    HV02 MOUSE
P01746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
NON TER
SEQUENCE
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Matches
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0921A6 MOI
1D 0921A
AC 0921D
DT 01-DD
DT 01-DD
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OC EUKB 1
OC EUKB 1
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TISSUB-LUNG;

TISSUB-LUNG;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,

A Altschul S.F., Jeederg B., Buetow K.H., Schafer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahy J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613; Stark S.E., Caton A.J.; Stark S.E., Caton A.J.; Stark S.E., Caton A.J.; Stark S.E., Caton A.J.; Stork S.E., Med. 174.613-624 (1991).

EMBL: U88667; AAR48044.1; -; mRNA.
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Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
MUCLEOTIDE SEQUENCE.
MEDLINE-99170165; PubMed=9509426;
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
"Cloning and characterization of CDNAs encoding VH and VL of a
monocolonal anti-CRA antibody (CRA 79) cross-reactive with NCA-95 and
generation of a single-chain FV molecule (SCFV).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AA; 26086 MW; 0276887248E9C771 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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Basembl; BNSWGS0000021155; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSPQS1_RAT PRELIMINARY;
QSPQS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYTFINYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S19965; S19965.
PIR; S19967; S19967.
PIR; S19968; S19968.
PIR; S26325; S26325.
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HV52 MOUSE
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAURHER R.L., Feingold B.A., Groue L.H., Derge J.G.,

Altschul S.P., Zeeberg B., Buctow K.H., Schaefer C.P., Bhat N.K.,

Altschul S.P., Zeeberg B., Buctow K.H., Schaefer C.P., Bhat N.K.,

Antschul S.P., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Antschul S.P., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Antschul S.P., Jordan H., Porents A.A., Rubin G.M., Hong L.,

Baptechen M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Anta S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratne P.H.,

A Kichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raber J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Recherzetion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Eukaryota, Metazoa, Chordontoglires, Glires, Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.2%; Score 50; DB 2; Length 475; 80.0%; Pred. No. 2.1; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR003106; Ig-like.
InterPro; IPR003106; Ig-MC.
InterPro; IPR003596; Ig-v.
Pfam; PP07654; Cl-set; 2.
SMART; SM00407; IG, 3.
SWART; SM00407; IG, 3.
SWART; SM00407; IGC, 1.
PROSITE; PS0939; IG_LIKE; 3.
PROSITE; PS0939; IG_MHC; UNGNOWN 2.
PROSITE; PS0939; IG_MHC; UNGNOWN 2.
SRQUENCE 475 AA; $\frac{5}{2}$118 MW; EC$\frac{6}{2}$1093E99996708 CRC64;
                                                                                                                                                                                                                                                                        NIH MGC Project;
Submitted (DRC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC087057; AAH87057.1; -; mRNA.
GO; GO:0003823; P:antigen binding; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSHZY6_MOUSE PRELIMINARY;
QSHZY6;
                                                                                                                                            sednences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYTPTNYGIN 10
                                                                                                                                                                                              [2]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOC544903 protein.
Name=LOC544903;
                                                                                                                                         and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4OUSE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10 haavy chain V region VH558 Al/A4 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Buarchoncoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
Yancopoulos G.D., Alt P.W.;
"Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region VH558 Al/A4. 
Framework-1. 
Complementarity-determining-1. 
Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                     Submitted (JAN-2015) to the EMBL/GenBank/DDBJ databases.

EMBL, BCO88837; AAH88837.1; -; mRNA.

R GO; GO:0003823; F:antigen binding; IEA.

R InterPro; IPR007110; Ig-11ke.

R InterPro; IPR003599; Ig c1.

R SMART; SM00409; IG ABC.

R SMART; SM00409; IG C1.

R R SMART; SM00409; IG C1.

R PR0SITE; PS00299; IG MRC; UNKNOWN 2.

R PROSITE; PS00299; IG MRC; UNKNOWN 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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SMR; P05327; 20-117.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR001596; Ig_v.
SMART; SM00406; IGV; 1.
PROSITE; PSS035; IG_LKB; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.0%; Score 47; DB 2;
80.0%; Pred. No. 7.4;
:1ve 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA.
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PIR; A02029; HVMSA1.
                                                         NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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49
54
68
68
85
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                                                                                                                NIH MGC Project;
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RESULT 8
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Altausherg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altachul R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldon M.F., Carainci P., Frange C.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carainci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shackchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                         Gaps
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NIH MGC Project;
Subhitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
-!- SUDGELDULAR LOCATION: Secreted (By similarity).
EMBL; BC091272; AAH91272.1; -; mRNA.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                          Score 46; DB 1; Length 117;
Pred. No. 2.7;
1; Mismatches 1; Indels
41 115 By similarity.
117 117
117 AA; 12971 MW; 8BOBC138856DFC9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              458 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
Ffam; PP07654; C1-8et; 3.
SMART; SM00409; IG; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain; Repeat. SEQUENCE 458 AA; 50161 MW;
                                                                                                                79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MX-2005 (TrEMBLrel. 30, 10-MX-2005 (TrEMBLrel. 30, 10-MX-2005 (TrEMBLrel. 30, LOC367586 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences."
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             22 RAT
QSBJZ2_RAT PRELIMINARY;
                                                                                                                                                                                                                                   1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                 45 GYTFTSYDIN 54
                                                                              Query Match
Best Local Similarity
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                           NON TER
SEQUENCE
DISULPID
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OCSBJ 28 Ag

OCSBJ 28 Ag

OCSBJ 10-M

DT 10-M

DE RALE

RA RALE

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MOI; WOI:96446; 194-4.

GO; GO:0003823; P:antiden binding; IDA.

GO; GO:001973; P:antiden binding; IDA.

GO; GO:001973; P:antiden binding; IDA.

GO; GO:001973; P:antibocterial humoral response (sensu Verte. . .; IDA.

GO; GO:001978; P:complement activation, classical pathway; IDA.

GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.

GO; GO:0006911; P:phagocytosis, engulation; IDA.

GO; GO:0006910; P:phagocytosis, recognition; IDA.

GO; GO:0006910; P:positive regulation of immune response; IDA.

GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.

GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.

GO; GO:000198; P:positive regulation of type I hypersensitivity; IDA.
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentía, Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB-Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Mammary tumor. Metallothionien-TGF alpha model. 10 month old
                                                       ö
Length 458;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (FRB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -; mRNA.
PIR; B45837; B45837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                          1,
     2;
                                                                                                                                                                                                                                                                                                  463 AA.
Score 46; DB 2
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Created)
                        Similarity 80.0%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                            Q99LC4 MOUSE
ID Q99LC4 MOUSE PRELIMINARY;
AC Q99LC4;
                                                                                                              1 GYTPTNYGIN 10
                                                                                                                                                                45 GYTFTNYDIH 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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SMR; Q99LC4; 21-459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
     Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Igh-4 protein.
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Pred. No. 4.4;

70.04;

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Best Local Similarity
Matches 7; Conserv
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065ZL3 9MURI
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MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

MALGADIS R.D., Felingold B.A., Grouse L.H., Derge J.G.,

Altechul S.P., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.P., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Helton D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

N. Helton B., Yourman J.W., Green B.D., Dickson M.C.,

Blakealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,

Rochnerch A., Schein J.B., Jones B.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae;
                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                  79.3%; Score 46; DB 2; Length 463; 70.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Lymph;
NIH WGC Project;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032733; AAH32733.1; -; mRNA.
HSSP; P01751; 1A6W.
SWR; Q6PILO; 20-117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 AA; 13913 MW; B76CB434F5A69788 CRC64;
                                                                                                                                                                                   463 AA; 51008 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                 2; Mismatches
       InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003596; Ig-v.
Pfan; PP07654; C1-set; 3.
SMART; SM00406; IGV; 1.
FMOSITE; PS5085; IG_LIKE; 4.
Immunoglobulin domain.
SEQUENCE 463 AA; 51008 MW;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SWART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lo human
Qepilo human preliminary;
Qepilo;
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                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                        1 GYTFTNYGIN 10
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Name=IGHV7-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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OGPILO HU

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DB 2; Length 125;

77.6%; Score 45;

Query Match

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MEDLINE-96269537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;

MEDLINE-96269537; PubMed=8699031; DOI=10.1016/0022-1759(96)00043-9;

Moell D., Bernardi T., Navarro-Teulon I., Marin M., Martinetto J.P.,

Noell D., Bernardi T., Pau B., Piechaczyk M., Biard-Piechaczyk M.;

"Analysis of the individual contributions of immunoglobulin heavy and

"Analysis of the binding of antigen using cell transfection and

"In plasmon resonance analysis.";

"I Immunol. Methods 193:177-187(1996).

RMBL; 882492; AAB37434.2; -; mRNA.

SMR, O652L3; 20-140.

RINGEPRO; IPR003599; Ig.

RINGEPRO; IPR003599; Ig.

RINGEPRO; IPR003596; Ig. V.

SMART; SM04409; IG; 1.

NR SMART; SM04406; IG; 1.

NR SMART; SM04406; IG; 1.

NR SMART; MO4406; IG; 1.

NR NR SMR; OFFICE SMR; NR SMR; OFFICE SMR; NR SMR; OFFICE 
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
   Gaps
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Dambreville C., Philippot L.;
Structure and activity of the denitrifying community in a maize planted soil fertilized with pig compost or ammonium nitrate.";
Submitted (APR-2005) to the BMBL/GenBank/DDBJ databases.
EMBL; DQ010807; AAY30755.1; -; Genomic_DNA.
InterPro; IPR001505; Copper_CuA.
InterPro; IPR001505; Copper_CuA.
FIREFPO; IPR001429; Cyt_C_Ox_2.
Pfam; PF00116; COX2; C
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       Indele
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13.SEP-2005 (TrEMBLrel. 31, Last sequence update)
13.SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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77.8%; Pred. No. 4.9;
tive 2; Mismatches
       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Created)
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Bacteria; environmental samples.
                                                                                                                                                                                                                                                                                                                                                                           25-0CT-2004 (TrEMBLrel. 28,
25-0CT-2004 (TrEMBLrel. 28,
25-0CT-2004 (TrEMBLrel. 28,
Tg10H (Fragment).
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ID Q4ZGV0_9BACT PRELIMINARY;
                                                                                                                                                                                                                                                                                                            Q65ZL3 9MURI PRELIMINARY;
Q65ZL3;
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Matches 7; Conservative
       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Butheria; Bu
Muridae; Murinae; Mus.
                                                                                                                                             54
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45 GYTPTSYGL 53
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                                                                             1 GYTFTNYGIN
                                                                                                                                             45 GYSPTTYGMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Tg10H;
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RAFFRS

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TISSUE-Mammary tumor metaatatized to lung. Tumor arose spontaneously;

KX TISSUE-Mammary tumor metaatatized to lung. Tumor arose spontaneously;

KX KEDLINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

KX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

KA Altschul S.F., Jordan H., Moore T., Max S.I., Mang J., Haileh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Haileh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Rand mouse ChNA servierses "...
                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CZECH II; TISSUB=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 468 AA; 51666 MW; 5BF6E527329F8461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 2;
Pred. No. 25;
1; Mismatches
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                                     Created)
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                                   (TrEMBLrel. 30, TrEMBLrel. 30, (TrEMBLrel. 30,
 OS69W9 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0-
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                                                                                      Hypothetical protein.
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                                 10-MAY-2005 (
10-MAY-2005 (
10-MAY-2005 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJNE=81053741; PubMed=6253904; Zakut R., Cohen J., Givol D.; "Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11."; Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS: This sequence was translated from an mRNA isolated from a myeloma that secretes 19G2b.
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                                                                                                        77.6%; Score 45; DB 2; Length 233; 70.0%; Pred. No. 8.1; 1: Mismatches 2; Indels
                                                                       26271 MW; 194F23F11497D008 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ensembl; ENSMUSGG000062635; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region.
DOMAIN 1 112 Ig-like.
                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Ig heavy chain V region MPC 11.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                             121 AA
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Nucleic Acids Res. 8:4839-4840(1980).
                                                                                                                                                                                                                                                                                                             PRT;
ProDom; PD000131; Copper CuA; 1.
PROSITE; PS50857; COX2 CUA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERRATUM, AND SEQUENCE REVISION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.,
8, Conservative
                                                                                                      Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
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190 GYCITNYGVN 199
                                                                                                                                                                                 1 GYTFTNYGIN 10
                                                        233
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GYTFTNYWI 34
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HSSP; P01751; 1NQB.
SMR; P01745; 1-121.
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                                                      233 2
233 AA;
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NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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P01745;
                                                    NON TER
SEQUENCE
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Q569W9_MOUSE
                                     NON TER
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HV01 MOUSE
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NEULINGATION SAUGHAND.

NEULINGATION Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S., Arakawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kanukawa T., Saito R., Ashburnar M., Batalov S., Casavant T., Redeta K., Matsuda H., Rabuchaman W., Gaasterland T., Gissi C., King B., Kochiwa H., Relschmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Redeta K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., Ga Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M., Anchone P., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Whitaker C., Whittaker C., Whittaker C., Whittaker C., Whittaker C., Whittaker Y., Suzuki H., Zoyo-oka K., Wang K.H., Weitz C., Whittaker C., Whitming L., Hynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Whittaka Y., Runctional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE-Pancreas; MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Muramatsu M., Hayashizaki Y., Muramatcu M., Hayashizaki Y., Muramatcu M., Hayashizaki Y., Eperanalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/61; IISSUE-Pancreas;
The RANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 day old male pancreas CDNA, RIKEN full-length enriched
11brary, clone:1810060009 product:immunoglobulin heavy chain 6 (heavy
chain of IgM), full insert sequence.
                                                                                                                                        Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J; TISSUE=Pancreas; MEDLINE-S9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-lengh cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
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WINTELEOTIDE SEQUENCE.

REDINE-20530913; Pubmed=11076861; DOI=10.1101/gr.152600;

REDINE-20530913; Pubmed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Pujiwake S., Inoue K., Togawa Y., Tanaka T., Matsuura E., Katahiki M.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001).
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Hara A., Hayatsu N., Hiramcko K., Hiranka T., Hori F.,
Hanagaki T., Hara A., Hayatsu N., Hiramcka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kosukawa T., Kato H.,
Nawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Rasuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Sakai C., Sakai K.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Lejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.; Rasunishi A., Yoshida K., Yoshino M.,
Bubmitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BRBL; AK007918; BAB25349.1; -; mRNA.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
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sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5EP-2005 (TrEMBLrel. 31, Created)
13.5EP-2005 (TrEMBLrel. 31, Last sequence update)
13.5EP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
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MGI; MGI:96443; Igh-la.
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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PIR; S26746; S26746.
HSSP; P01864; 1BOG.
SWR; Q9D8L4; 20-469.
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NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

TISSUE-mammary gland;

NEDINEL-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Angleton M., Soares M.B., Bonaldo M.F., Gasvant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wiskin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wokernan R.J., Mark J.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Allalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Warra M.A.,

Butterfield Y.S.N., Warra M.A
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InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig.
InterPro; IPR003066; Ig_MIC.
InterPro; IPR003596; Ig_WIC.
InterPro; IPR003596; Ig_W.
InterPro; IPR003596; Ig_W.
InterPro; IPR00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
RP0SITE; PS00290; IG_MIC; UNKNOWN_3.
RPOSITE; PS00290; IG_MIC; UNKNOWN_3.
RPOSITE; PS00290; IG_MIC; UNKNOWN_3.
RPOSITE; PS00290; IG_MIC; UNKNOWN_3.
SEQUENCE 590 AA; 64892 MW; D425318F9A188B14 CRC64;
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO96667; AAH96667.1; -; mRNA.
MGI; MGI:96448; Igh-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Muroidea; Muridae; Murinae; Mus.
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Matches 8; Conservative
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TISSUE=Mammary gland;
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Search completed: April 25, 2006, 06:24:37 Job time : 55.3962 secs

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Sequence 110, App
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                                                                                                                                                                                                                        April 25, 2006, 06:25:05; Search time 13.4906 Seconds (without alignments) 61.284 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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(cgn2_6/ptodata/1/iaa/5_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6_COMB.pep:*
(cgn2_6/ptodata/1/iaa/H_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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58
1 GYTFTNYGIN 10
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Appl Appl Appl App App App App App App A		
10044, 64, 64, 64, 64, 64, 64, 64, 64, 64,		Gaps
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248884444464464666 808844444646	DIES 69	DB 2; 0.052;
4224-4224-4224-4224-4224-4224-4224-422	%TS BODII 9.469	110: 18; D
15-08-082-842A-28 15-08-082-842A-88 15-08-082-842A-88 15-08-082-842A-88 15-08-082-942A-89 15-08-139-765-124 15-08-136-389-126 15-09-116-389-126 15-09-11-485-126 15-09-11-485-126 15-09-711-485-126 15-09-711-485-126 15-09-711-485-126 15-09-711-485-126 15-09-711-485-126 15-09-018-136-136 15-09-018-136-136 15-09-018-136-136 15-08-018-469-108 15-08-908-469-108	ALIGNMENTS 469 G. G. G. I.44 Mb f ttble Sco Sco Sco Sco Nol/1001 001 001 001 001 001 001 001 001 00	un 24 10
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US-08-08-08-08-08-08-08-08-08-08-08-08-08-	ALIGNMENTS ALIGNMENTS  n US/08908469  n US/08908469  Adames A. I. Leconard G. Y. Vonne M. N: ANTI-VEGF ANTIBODD  N: FES: 131  DRESS: Henry B. INCRES: He	g ö
	Manuel  Manuel  Manuel  Manuel  Young  Manuel  Manuel	00
1118 1118 1118 1118 1118 1118 1118 111	LOS HILLS OF THE STANKING SET OF THE CONTROL OF THE SET	ig ig
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	SULT 1 -08-908-469-110 Sequence 110, Applicat GENERAL INFORMATION: GENERAL INFORMATION: BEES LOWING HELL TITLE OF INVENT NUMBER OF ENGUE CORRESPONDENCE ADDRESSERS: STREET: 1 CITY: SOUL CONFUTER: Cal CONFUTER: Cal COMPUTER: P4080 COMPUTER: P4080 COMPUTER: Cal CAL CAL TELEPONE: CAL TELEPONE: CAR TELEPON	SEQUENC -08-908-469-11 Query Match Best Local Sim
	LT 1 8-908-465 tent No. GENERAL GENERAL NUME CORI CORI TITI NUME TITI TITI TELI	ω Σ Ωα
00000000000000000000000000000000000000	RESULT US-08-9 US-08-9 GEN GEN INF	-08-908 Query M Best Lo Matches
	80	Sn

Sequence Sequence

Sequence

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APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Gross, Mitchell
APPLICANT: Fourtenestein, Giora
APPLICANT: Padlan, Eduardo
APPLICANT: Padlan, Rubardo
APPLICANT: Padlan, Rubardo
APPLICANT: Padlan, Rubardo
APPLICANT: Padlan, Rubardo
APPLICANT: Padlan, Aumbhai
APPLICANT: Padlan, Rubardo
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.8%; Score 55; DB 2; Length 10; 90.0%; Pred. No. 0.013; 1ive 1; Mismatches 0; Indels
                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CLI, Steven X.
REGISTRATION NUMBER: 44,637
REPRENCE/DOCKET WINDER: P1093P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8614
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 84, Application US/08783853A Patent No. 6005091 GENERAL INFORMATION:
                                        CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 90.0.
Best Local Similarity
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Com
OPERATING SYSTEM:
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US-08-783-853A-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION SATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 44,637
REFERENCE/DOCKET NUMBER: 91093P1
TELECOMPUNICATION INFORMATION:
TELECOMPUNICATION INFORMATION:
                                                                                                                                                                                                                         APPLICANT: Baca, Manuel
Wells, James A.
Fresta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                                                                                                                                   US-08-908-469-114
; Sequence 114, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 118 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 10; Conservative
1 GYTFTNYGIN 10
                     26 GYTFTNYGIN 35
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Gaps

Gaps

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APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Crusch, William
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Patel, Andrew
APPLICANT: Patel, Arubhai
APPLICANT: Patel, Arubhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: ANTICOAGULANT
CORRESPONDENCE ADDRESS:
ADDRESSER: ADDRESS:
ADDRESSER: ADDRESS:
ADDRESSER: ADDRESS:
ADDRESSER: SmithKilme Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                            Length 92;
                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                          Score 55; DB 2;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
CORENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: APPLICATION NUMBER: 60/029,119
FILING DATE: APPLICATION NUMBER: P50438
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEFRIONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08783853A Patent No. 6005091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERIFICS:
IENGTH: 112 amino acids
TYPE: amino acid
FELECOMMUNICATION INFORMATION:
                                                                              84:
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                          INPORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                TELEPHONE: 610-270-5096
TELEFAX:
                                                                                                                                                                                                                                                           FRAGMENT TYPE: internal ORIGINAL SOURCE: US-09-344-050-84
                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GYTFTNYGMN 12
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USA
                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-783-853A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: PA
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; Sequence 84, Application US/09344050
; Patent No. 6391299
; GENERAL INFORMATION:
   APPLICANT: Blackburn, Michael
   APPLICANT: Church, William
   APPLICANT: Church, William
   APPLICANT: Gross, Michell
   APPLICANT: Padlan, Eduard
   APPLICANT: Padlan, Eduard
   APPLICANT: Patel, Annubal
   APPLICANT: Sylvester, Daniel
   TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
   TITLE OF INVENTION: OF THROMBOSIS
   NUMBER OF SEQUENCES: 111
   CONTRESPONDENCE ADDRESS:
   ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEB: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.8%; Score 55; 90.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER TRADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: EM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumetater. Kirk
REGISTRATION NUMBER: 33,833
REGISTRATION NUMBER: 33,833
    CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
PILING DATE: 24-OCT-1996
ATVORBY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REPERRENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                   84:
                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GYTPTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: 11 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-783-853A-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-344-050-84
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Gaps

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Sequence 124, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Process
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall: O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                   94.8%; Score 55; DB 2; Length 112; 90.0%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.8%; Score 55; DB 1; Length 118; 90.0%; Pred. No. 0.15; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sars Tower, 233 South Wacker Drive CITY: Chicago Sars Tower, 233 South Wacker Drive CITY: Chicago Sars Tower, 233 South Wacker Drive STATE: 111inois COUNTRY: USA ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: PLOSPY disk COMPUTER: IBM PC COMPATIBLE OPERATION SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/425,336 PRIOR APPLICATION NUMBER: 08/064,691 PRIOR APPLICATION NUMBER: 08/064,691 PRIOR APPLICATION NUMBER: 08/07/901,707 PRIOR APPLICATION NUMBER: US/07/901,707 PRIOR EFFERNICE/COCKET NUMBER: 33294 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION INFOR
                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 90.0.
Best of 9; Conservative
                      Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                               1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYTFTNYGIN 10
                                                                                                                                                                                                     23 GYTFTNYGMN 32
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                                                                                                                                                                                                                                                                                                 RESULT 8
US-08-425-336-124
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; Sequence 20, Application US/09344050
; Sequence 20, Application US/09344050
; Patent No. 6391299
; GENERAL INFORMATION:
    APPLICANT: Church, William
    APPLICANT: Church, William
    APPLICANT: Peuerstein, Giora
    APPLICANT: Peuerstein, Giora
    APPLICANT: Padlan, Eduardo
    APPLICANT: Patel I, Arunbai
    APPLICANT: Patel I, Arunbai
    APPLICANT: Sylvester, Daniel
    ITILE OF INVENTION: OF THROWBOSIS
    ITILE OF INVENTION: OF THROWBOSIS
    ITILE OF SEQUENCES: II
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Gmithkline Beecham Corporation
    STREET: 709 Swedeland Road
    CITY: King of Prussia
    STATE: PA
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                        94.8%; Score 55; DB 2; Length 112; 90.0%; Pred. No. 0.14; tive 1; Mismatches 0; Indels
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ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
APPLICATION NUMBER: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFENCE/DOCKET NUMBER: 950438
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
CORIGINAL SOURCE:
US-08-183-853A-20
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Inear MOLECULE TYPE: protein HYPOTHETICAL: NO
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                 1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                          23 GYTFINYGMN 32
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) ORIGINAL SOURCE:
US-09-344-050-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
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Gaps
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Sequence 126, Application US/08488113B
Sequence 126, Application US/08488113B
Sequence 126, Application US/08488113B
Sequence 126, Application
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSER: MCANDERW, Held & Malloy, Ltd.
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Pred. No. 0.15;
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                                                                                              NIAME: MCNICHOLAS, Janet M.

REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPLORS: 312/707-8889
TELEPAX: 312/707-9155
TELEPAX: 312/707-9155
TELERAX: 312/707-9155
TELERAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 124:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
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500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GYTFTNYGIN 10
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
Chicago
: Illinois
RY: USA
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                                                                                  60661
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Sequence 124, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Setter, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSES: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
  Sequence 126, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proceins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: ILLINOIS
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSPY disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC COMPA:
COMPUTER: IBM FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION NUMBER: US/08/04,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
RILING DATE: 19-JUN-1992
RILING DATE: 10-JUN-1991
ATTORNEY/AGENT INFORMATION:
NUMBE: MEYERS THORWATION:
NUMBE: MEYERS THOR
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Pred. No. 0.15;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REPERENCE DOCKET NUMBER: 31394
TELECOMMUNICATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-648
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INPORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYTFTNYGIN 10
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                                                                                                                                                                                                                                                                                                                        STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-488-113B-124
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LENGTH: 118 amino acids
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 GYTFTNYGMN 35
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| Sequence 124, Application US/08477484B
| Sequence 124, Application US/08477484B
| Patent No. 575663B
| Patent No. 575663B
| Patent No. 575663B
| APPLICANT: Better, Marc D. APPLICANT: Studnika, Gary M. APPLICANT: Studnika, Gary M. ITTLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins Information Proteins NCHABER OF SEQUENCES: 169
| CORRESPONDENCE ADDRESS: ADDRESSE: MCANdrews, Held & Malloy, Ltd. STREET: 500 West Madison Street, 34th floor CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-DUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-DUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: US-DUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US-DUN-1992
RADELCATION NUMBER: US 07/787,567
FILING DATE: US-DUN-1992
RADELCATION NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION NUMBER: 1102ZUS07/200-70.P3.C2A
TELECOMMUNICATION NUMBER: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11022US07/200-70.P3.C2A
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB 1,
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.8%;
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LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GYTFTNYGIN 10
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| PRIOR PERICATION | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190 | 190
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Sequence 29, Application US/08107669D

Sequence 29, Application US/08107669D

Patent No. 5766886

GENERAL INFORMATION:
APPLICANT: Studnick, Gary M.
TILLS OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20065-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
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Pred. No. 0.15;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              Length 118;
                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/107,669D

FILING DATE: 13-AuG-1993

CLASSIFICATION TABER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIOR APPLICATION NUMBER: CS 07/808,464

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: MICHEL A. DEC-1991

ATTORNEY/AGENT INFORMATION:

NEGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 30,931

INFORMATION FOR SEQ ID NO: 29:

INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                       Score 55; DB 1;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                          TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acide
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.8%;
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amino acid
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Best Local Similarity 90.0
Matches 9; Conservative
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LENGTH: 118 amino aci
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Best Local Similarity
Matches 9; Conserv
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US-08-107-669D-29
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US-08-107-669D-28
Sequence 28, Application US/08107669D
Sequence 28, Application US/08107669D
Sequence 28, Application US/08107669D
Sequence 28, Application
Sequence 28, Application
TITLE No. 576686
GENERAL Studnicka, Cary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES:
ADDRESSER: Sterne, Kessler, Goldstein and Fox P.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BREENIN PC-DOS/MS-DOS
SOFTWARE: Breenin Release #1.0, Version #1.25
CUASSIFICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AQC-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: BO7/808,464
FILING DATE: 14-DEC-1991
FILING DATE: 14-DEC-1991
FILING DATE: 13-DEC-1991
FILING DATE: 13-DEC-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 1; Length 118; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 0; Indels
PILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCMAIGHOLBS, Janet M.
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 31,707-9155
TELLEPRONE: 312/707-9155
TELLEPRONE: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENUTH: 118 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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RESULT 14

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Search completed: April 25, 2006, 06:28:38 Job time : 13.4906 secs

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112, App
112, App
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Sequence 116, App
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                                                                                                                                     April 25, 2006, 06:58:17 ; Search time 43.5849 Seconds (without alignments) 95.866 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-056-160B-110
US-09-056-160B-114
US-10-234-671-110B
US-10-633-043-11
US-10-974-591-10B
US-10-974-591-112
US-10-974-591-12
US-10-637-995-12
US-10-64-42B-11
US-10-744-42B-11
US-10-764-42B-11
US-10-764-42B-11
US-10-764-42B-11
US-10-766-852-10
US-10-766-852-10
US-10-706-852-10
US-10-234-671-1
US-10-234-671-1
US-10-234-671-1
US-10-234-671-1
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                                                                                                                                                                                                                                                                                                                                                                                               1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                  1 GYTFTNYGIN 10
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                                                                                              OM protein
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Sequence 14, Application US/10764428

Sequence 14, Application No. US20040229310A1

GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
TITLE OF INVENTION: TIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
TITLE OF INVENTION: CULTURE
TITLE OF INVENTION: 11669-120USU

CURRENT PILING DATE: 2004-01-23

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PALENTIN VERSION 3.1

LENGTH: 10
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                   884,
884,
820,
500,
500,
500,
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Sequence 1
Sequence 2
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                       seguence
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Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 10, Conservative 0; Mismatches 0; Indels
      US-09-965-099-84
US-10-051-852-84
US-10-681-421-84
US-09-965-099-20
US-10-681-421-84
US-10-681-421-84
US-10-830-899-50
US-10-830-899-50
US-10-861-662-50
US-10-861-662-50
US-09-971-543-8
US-09-971-543-8
US-09-971-543-8
US-09-971-543-8
US-09-971-543-8
US-09-971-543-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 110, Application US/09056160B
; Sequence 110, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Presta, Leonard G.
APPLICANT: Dowman, Henry B.
APPLICANT: Cownen, Yeonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA May
CITY: South San Francisco
; STATE: California
                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: HVR1 residues 26-35
US-10-764-428-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYTFTNYGIN 10
RESULT 2
US-09-056-160B-110
                                                                                                                                                                                                                                                                                                       US-10-764-428-14
 FEATURE:
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100.0%; Score 58; DB 3; Length 118; 100.0%; Pred. No. 0.094;
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TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-889-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/056160
APPLICATION NUMBER: 00/126446
FILING DATE: 07-APR-1998
APPLICATION NUMBER: 60/12646
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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TOPOLOGY: Linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-234-671-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 108, Application US/10234671
Publication No. USZ0030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
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TELEPHONE: 650/225-8674
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
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TYPE: Amino Acid
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NAME: Cui, Steven X.
TELEPHONE: 650/225-1896
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                TOPOLOGY: 114 amino acids
TOPOLOGY: 1.1-1
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GYTFTNYGIN 10
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                                                                                                                                                                                                                                                                                                US-09-056-160B-114
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US-10-234-671-108
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MEDIUM TYPE: 35. inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOGTWARRE: WinPatin (Genentech) CURRENT APPLICATION DATA: (Genentech) APPLICATION DATA: (ASPLICATION TOWER: US/09/056,160B FILING DATE: 06-Apr-1998 CLASSIFCATION: 424 PRIOR APPLICATION NUMBER: 60/054,856 FILING DATE: 06-AUG-1997 ATTOMNA DATE: 06-AUG-1997 ATTOMNA DATE: 06-AUG-1997 ATTOMNA INFORMATION: NAME: HABBAK, Janet E. REGISTRATION WUMBER: 28,616 PRIOR PROPERTY NUMBER: 28,616 PRIOR PRIOR PRIOR
                                   ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-APF-1998
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Fatent No. US20020032315A1
GENERAL INFORMATION:
BAPPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
Cowman, Henry B.
APPLICANT:
APPLI
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, JANEL E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECPMUNICATION INFORMATION:
TELECPMONE: 650/225-1896
TELEPAX: 650/325-9881
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
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P1093R2
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Best Local Similarity 100.
Matches 10; Conservative
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US-09-056-1608-110
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             COUNTRY:
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Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 10; Conservative 0; Mismatches 0; Indels
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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FELEFAX: 650/952-988
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SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                26 GYTFINYGIN 35
                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-10-683-043-11
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                                                                                                                  SEQ ID NO 11
LENGTH: 118
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APPLICANT: Perrara, Napoleone
TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
TITLE OF INVENTION: and Uses Thereof
PILE REPERENCE: P1717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER KEADABLE FORM:
COMPUTER TABLABLE FORM:
COMPUTER: 15.5 inch, 1.44 Mb floppy disk
COMPUTER: 15.5 inch, 1.64 Mb floppy disk
COMPUTER: 15.5 inch, 1.64 Mb floppy disk
COMPUTER: 15.5 inch, 1.65 inch
SOFTWARE: 16.5 inch
SOFTWARE: 16.5 inch
APPLICATION NUMBER: 16.7 inch
FILING DATE: 0.5 inch
APPLICATION NUMBER: 0.0/12646
FILING DATE: 0.6 inch
APPLICATION NUMBER: 0.0/12646
FILING DATE: 0.7 inch
APPLICATION NUMBER: 0.0/12646
FILING DATE: 0.7 inch
APPLICATION NUMBER: 0.0/12646
FILING DATE: 0.6 inch
APPLICATION NUMBER: 0.0/12646
FILING DATE: 0.6 inch
APPLICATION NUMBER: 6.0/12646
FILING DATE: 0.0 inch
APPLICATION NUMBER: 9.0/12646
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                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-234-671-112
                                                                                                                                                Sequence 112, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-683-043-11

i Sequence 11, Application US/10683043

i Publication No. US20050053599A1

i GENERAL INFORMATION:
                                                                                                                                                                                                                                                             Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
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INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
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COMPUTER READABLE FORM:
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-10-234-671-112
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                                                                                                                                                                                                                                                          100.0%; Score 58; DB 5; Length 118; 100.0%; Pred. No. 0.094; tive 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/974,591
FILING DATE: 50-004
CLASSIFICATION: CURRINGWID
PRIOR APPLICATION NUMBER: 06/73750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSE: Genettech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P1093P1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/683,043
CURRENT FILING DATE: 2003-10-09
PRICA APPLICATION NUMBER: US/09/218,481
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27-NOV-2000
APPLICATION NUMBER: 08/908469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/833504
FILING DATE: 07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/723752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 108, Application US/10974591
Publication No. US20050112126A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 118 amino acida TYPE: Amino Acid
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240 GYTFTNYGIN 249
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Publication No. US20050048572A1;
GENERAL INFORMATION:
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING ANTIBODY PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Witheatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/974,591
FILING DATE: 26-Oct-2004
CLASSIPICATION ATA:
APPLICATION NUMBER: 09/723752
FILING DATE: 27-NOV-2000
APPLICATION NUMBER: 08/808469
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cul, Steven X,
REFERENCE/DOCKET NUMBER: 91093PIDICI
TELECOMMUNICATION INFORMATION:
NAME: Cul, Steven X,
REFERENCE/DOCKET NUMBER: 91093PIDICI
TELECOMMUNICATION INFORMATION:
NAME: CUL, Steven X,
REFERENCE/DOCKET NUMBER: 91093PIDICI
                                                                                                                                       Sequence 112, Application US/10974591
Publication No. US20050112126A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
COMEN, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 112: US-10-974-591-112
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 118 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
COUNTRY: USA
                   26 GYTFINYGIN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GYTFTNYGIN 10
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GYTPINYGIN 10
                                                                                                                              US-10-974-591-112
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                                                                                                     RESULT 8
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; OTHER INFORMATION: The first 214 amino acids are the light chain followed by the ; OTHER INFORMATION: heavy chain beginning at position 215 (E).
US-10-764-428-5
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Publication No. US20040229310A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: WETHOOS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING

TITLE OF INVENTION: CULTURE

TITLE OF INVENTION: CULTURE

TITLE OF INVENTION: US/10/764,428

CURRENT APPLICATION NUMBER: US/10/764,428

CURRENT APPLICATION NUMBER: US 60/442,484

PRIOR PILING DATE: 2003-01-23

PRIOR PILING DATE: 2003-01-23

PRIOR SEQ ID NOS: 33

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PALCHING VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10764428
Publication No. US20040229310A1
GENERAL INFORMATION:
APPLICANT: Simmons, Laura
TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
TITLE OF INVENTION: CULTURE
TITLE OF INVENTION: CULTURE
FILE REFERENCE: 11669-120UGH
CURRENT APPLICATION NUMBER: US/10/764,428
CURRENT APPLICATION NUMBER: US/04-01-23
PRIOR FILING DATE: 2004-01-23
PRIOR FILING DATE: 2003-01-23
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                                                                                                                                                                                                                                                                                                                                                                                    Score 58; DB 5; Length 479;
Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
FILE REFERENCE: 11669.195USU1
CURRENT APPLICATION NUMBER: US/10/697,995
CURRENT FILING DATE: 2003-10-30
FRIOR APPLICATION NUMBER: US 60/422,952
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 12
LENGTH: 479
TYPE: PRT
                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Anti-VEGF heavy chain
US-10-697-995-12
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0,
                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence
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SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 670
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Query Match
Best Local Similarity 90...
Best Local 9; Conservative
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US-10-706-852-2
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Sequence 11, Application US/10764428

Sequence 11, Application Wo. US20040229310A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING

TITLE OF INVENTION: WILLD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL

TITLE OF INVENTION: CULTURE

TITLE OF INVENTION: CULTUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Light chain starts at residue 1 (D); Heavy chain starts at ; OTHER INFORMATION: residue 215 (Q)
; SEQ ID NO 9
; LENGTH: 670
; TYPE: PAT
; TYPE: PAT
; PEATURE:
; FEATURE:
; OTHER INFORMATION: Light chain starts at residue 1 (D); Heavy chain starts at
; OTHER INFORMATION: residue 215 (Q)
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100.0%; Pred. No. 0.49;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      0; Indels
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ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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| OCHER INFORMATION: 143pt. chiin cearte at residue 1 (0); Heavy chain cearte at 193-10-1744-428-27
| Usery March | Usery March
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PRIOR FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 09/965,796
PRIOR APPLICATION NUMBER: 09/307,816
PRIOR APPLICATION NUMBER: 09/307,816
PRIOR PILING DATE: 1999-05-10
PRIOR PILING DATE: 1999-05-10
PRIOR PILING DATE: 2003-01-24
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-01
PRIOR PILING DATE: 2003-03-01
PRIOR PILING DATE: 2003-04-01
PRIOR PILING DATE: 2003-06-17
NUMBER OF EGQ ID NOS: 21
SOFTWARE: PATENTING VIRIABLE
PRIOR PILING DATE: 2004-06-17
NUMBER OF EGG ID NOS: 21
SOFTWARE: PATENTING NUMBER: 60/478,830
PRIOR PILING DATE: 2004-06-17
NUMBER OF EGG ID NOS: 21
PRIOR PILING DATE: 2004-06-17
NUMBER OF EGG ID NOS: 21
PRIOR PILING DATE: 2004-06-17
NUMBER OF EGG ID NOS: 21
PRIOR PILING DATE: 2004-06-17
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PRIOR PILING
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98.3%; Score 57; DB 5; Length 120;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 1; Mismatches 0; Indels
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26 GYTFTNYGVN 35
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Search completed: April 25, 2006, 07:08:46 Job time : 44.5849 secs

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April 25, 2006, 07:01:21 ; Search time 6.41509 Seconds (without alignments) 68.593 Million cell updates/sec
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1. /SIDSS/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

2. /SIDSS/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3. /SIDSS/ptodata/1/pubpaa/USO7 NEW_PUB.pep:*

4. /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5. /SIDSS/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*

7. /SIDSS/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*

7. /SIDSS/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*

8. /SIDSS/ptodata/1/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             225428 Beqs, 44002918 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                      US-10-764-428-14
58
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	11,	Sequence 84, Appl	20	~	4	Sequence 6, Appli	Sequence 17, Appl	18	Sequence 19, Appl	Sequence 20, Appl	21,	22,	23,	24,	22,	5 6	35,	32	6	14	15,	7, 4	-		Sequence 111, App
SOMESTERS	σι	US-10-648-816-11	US-11-240-195-84	US-11-240-195-20	US-11-174-186-2	US-11-174-186-4	US-11-174-186-6	US-11-174-186-17	US-11-174-186-18	US-11-174-186-19	US-11-174-186-20	US-11-174-186-21	US-11-174-186-22	US-11-174-186-23	US-11-174-186-24	US-11-174-186-25	US-11-174-186-26	US-11-174-186-35	US-11-037-199-32	US-10-648-816-9	US-10-648-816-14	US-10-648-816-15	US-11-240-195-7	US-11-240-195-31	US-11-240-195-52	US-11-240-195-111
	DB	9	۲	7	7	7	7	-	7	7	7	7	7	7	7	7	7	7	7	ø	ø	9	7	7	7	7
	Query Match Length	118	92	112	116	116	116	116	116	116	116	116	116	116	116	116	116	117	117	118	118	121	121	121	121	121
*	Query Match	100.0	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8	94.8
	Score	58	55	55	55	55	55	55	55	55	សួ	SS	55	55	55	55	55	55	55	55	55	55	55	55	55	55
	Result No.	-	7	m	4	S	v	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence Sequence
123 7 US-11-240-195-109 123 7 US-11-208-422-8 140 7 US-11-208-422-10 140 7 US-11-240-195-89 579 7 US-11-174-186-41 247 7 US-11-054-515-188 247 7 US-11-054-515-2126 247 7 US-11-054-515-2126 247 7 US-11-266-444-188 247 7 US-11-266-444-2126 247 7 US-11-266-444-2126 247 7 US-11-266-444-2126	248 7 US-11-054-515-1008 248 7 US-11-266-444-1008 249 7 US-11-054-515-2078 249 7 US-11-054-515-2078 249 7 US-11-266-444-1897 249 7 US-11-266-444-2078 253 7 US-11-054-515-1530
	53 91.4 53 91.4 53 91.4 53 91.4 53 91.4

ALIGNMENTS

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US-10-648-816-11

US-10-648-816-11

Sequence 11, Application US/10648816

Publication No. US20050244405A1

GENERAL INFORMATION:

APPLICANT: Van Bruggen, Nicholas

APPLICANT: Perrara, Napoleone

TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists

TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists

TITLE OF INVENTION: Vand Uses Thereof

TITLE OF INVENTION NUMBER: US/10/648,816

CURRENT PILING DATE: 2000-11-21

PRIOR FILING DATE: 2000-11-21

PRIOR FILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 11
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| Sequence 84, Application US/11240195 |
| Sequence 84, Application US/11240195 |
| Sequence 84, Application NO. US20060057140A1 |
| GENERAL INFORMATION: APPLICANTION: APPLICANT: PEUERERICS |
| TITLE 0P INVENTION: APTICOAGULANT AGENTS USEFUL IN TREATMENT |
| TITLE 0P INVENTION: APPLICANTION APPLICANTON: OF THROMBOSIS |
| TITLE 0P INVENTION: APPLICANTON NUMBER: US/11/240,195 |
| CURRENT PILING DATE: 2005-09-30 |
| PRIOR APPLICATION NUMBER: US/10/430,176 |
| PRIOR PILING DATE: 2003-05-05 |
| PRIOR PILING DATE: 2003-05-05 |
| PRIOR PILING DATE: 2003-03-05 |
| PRIOR PILING DATE: 2003-05-05 |
| PRIOR PILING DATE: 2003-03-05 |
| PRIOR PILING DATE: 2003-05 |
| PRIOR
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Best Local Similarity 100.0%; Score 58; DB 6; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 GYTFTNYGIN 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Homo sapiens
US-10-648-816-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Sequence 2, Application US/11174186, Publication No. US20050244418A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 GYTFTNYGMN 35
       23 GYTFTNYGMN 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-11-174-186-4
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APPLICANT: Fencration, Giora Z.

TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT ITLES OF INVENTION: OF THROMBOSIS

FILE REFERENCE: FOOGL-1

CURRENT APPLICATION NUMBER: US/11/240,195

CURRENT APPLICATION NUMBER: US/11/240,195

CURRENT APPLICATION NUMBER: US/11/240,176

PRIOR PILING DATE: 2003-05-05

PRIOR PILING DATE: 2003-05-05

PRIOR PILING DATE: 2003-05-05

PRIOR PILING DATE: 1999-07-22

PRIOR APPLICATION NUMBER: 09/359,202

PRIOR PILING DATE: 1998-08-07

PRIOR PILING DATE: 1997-01-06

PRIOR PILING DATE: 1997-01-06

PRIOR PILING DATE: 1997-01-06

PRIOR PILING DATE: 1996-01-17

PRIOR PILING DATE: 1996-10-24

PRIOR PILING DATE: 1996-10-24

NUMBER OF SEQ ID NOS: 111

SOFTWARE: PSECED ID NOS: 111

LEWATH: 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.8%; Score 55; DB 7; Length 92; 90.0%; Pred. No. 0.016; Live 1; Mismatches 0; Indels
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 60/095,714
PRIOR PILING DATE: 1998-08-07
PRIOR PLING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 10/051,852
PRIOR PILING DATE: 2002-01-17
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-01-06
PRIOR PILING DATE: 1997-01-06
PRIOR PILING DATE: 1996-01-17
PRIOR PILING DATE: 1996-01-17
PRIOR PILING DATE: 1996-01-17
PRIOR PILING DATE: 1996-01-17
PRIOR PILING DATE: 1996-10-24
NUMBER OF SEQ ID NOS: 111
SUGTWARRE: PRAESER FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/11240195 Publication No. US20060057140A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-11-240-195-84
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US-11-240-195-20
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1 GYTFINYGIN 10

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Sequence 4, Application US/11174186

Sequence 4, Application US/11174186

Publication No. US20050244418A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Glilies, Stephen
APPLICANT: Glilies, Stephen
APPLICANT: Glan, Xiugi
APPLICANT: Glan, Xiugi
TITLE NETERENCE: LEX.019
CURRENT PLICH DATE: 2005-07-01
FRICR PILING DATE: 2005-07-01
PRIOR PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 116
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LOCATION: (2)._(2)
OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (9). (9). (9) OTHER INFORMATION: wherein Xaa at position 9 is a proline or an alanine
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Gial, Kin-Ming

APPLICANT: Gial, Xiudi

TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

FILE REPERENCE: LEX-Oil

FILE REPERENCE: LEX-Oil

CURRENT APPLICATION NUMBER: US/11/174,186

CURRENT FILING DATE: 2005-07-01

PRIOR PAPLICATION NUMBER: US 60/288,564

PRIOR FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PARCENT Version 3.3

SEQ ID NO 2

LENGTH: 116
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OTHER INFORMATION: wherein Xaa at position 11 is a leucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEATURE:
OTHER INFORMATION: variable heavy chain sequence in the EpCAM antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.8%; Score 55; DB 7; Length 116; Best Local Similarity 90.0%; Pred. No. 0.02; Matches 9; Conservative 1; Mismatches 0; Indels
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LOCATION: (16)..(16)
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NAME/KEY: misc feature
LOCATION: (100)..(100)
OTHER INFORMATION: wherein Xaa at position 100 is an isoleucine or a methionine
                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1087..(108)
OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine
                                                                                                                                                                                                                                                                                                                            LOCATION: (91)..(91)
OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-ULITY-186-6

Sequence 6, Application US/11174186

Sequence 6, Application US/11174186

Publication No. US20050244418A1

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Gillies, Stephen
APPLICANT: Qian, Xiugh

TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION WUMBER: US/11/174,186

CURRENT FILING DATE: 2005-07-01

PRIOR FILING DATE: 2005-07-01

PRIOR FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42

SEQ ID NO 6

TIMES: PRIOR FILING DATE: 116

TIMES: PRIOR FILING DATE: 2001-05-03

SEQ ID NO 6

TIMES: RESERVED TO 1005-03

TIMES: PRIOR FILING DATE: 2001-05-03

SEQ ID NO 6

TIMES: RESERVED TO 1005-03

TIMES: RESERVED TO 1005-03
                                                       LOCATION: (85)...(85)
OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (2). (2)
OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature; LOCATION: (111)..(111); OTHER INFORMATION: wherein Xaa at position 111 is a serine or a threonine US-11-174-186-4
                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (93)...(93)
OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(9)
OTHER INFORMATION: wherein Xaa at position 9 is a proline or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 7;
Pred. No. 0.02;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEATURE: OTHER INFORMATION: heavy sequence consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GYTFTNYGIN 10
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NAME/KEY: misc_feature
LOCATION: (11)..(11)
                                                                                                   misc_feature
(85)..(85)
                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:
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LOCATION: (69)...(69)
OTHER INFORMATION: wherein Xaa at position 69 is an alanine, a threonine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TION: (73)...(73)
R INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (70) ... (70)
OTHER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (80) .. (80)
OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /KEY: msic_feature
TION: (63) ... (63)
R INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (68)..(68)
OTHER INFORMATION: wherein Xaa at position 68 is a phenylalanine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /KEY: misc_feature
TION: (46) ... (46)
R INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
INFORMATION: wherein Xaa at position 16 is a glutamic acid or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (84)...(84)
OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (76)...(76)
OTHER INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
                                                                                                                                                                                                                                                                                                                                     LOCATION: (40)..(40)
OTHER INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (72)...(72)
OTHER INFORMATION: wherein Xaa at position 72 is a leucine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (79)... (79) OTHER INFORMATION: wherein Xaa at position 79 is an alanine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (65)...(65)
OTHER INFORMATION: wherein Xaa at position 65 is a lysine or a glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATION: (71)..(71) wherein Xaa at position 71 is a serine or a threonine
                                                                                                            OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: (43)...(43)
INFORMATION: wherein Xaa at position 43 is a lysine or a glutamine
                                                                                                                                                                                                                     ION: (38)..(38)
INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ON: (83). (83) INFORMATION: wherein Xaa at position 83 is an isoleucine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
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                                                                                                                                                       PEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                      NAMB/KEY: misc_feature
LOCATION: (40)...(40)
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                                                                 NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc feature
LOCATION: (108)...(108)
COTHER INFORMATION: wherein Kaa at position 108 is a glutamine or a threonine
US-11-174-186-6
                                                                                                                                                                                                                                                                                                                                                                                                                                         ## Sequence 17, Application US/11174186

## Sequence 17, Application US/11174186

## Publication No. US20050244418A1

## REPERENT ON. US20050244418A1

## APPLICANT: Gillies, Stephen

## APPLICANT: LEX-019

## CURRENT APPLICATION NUMBER: US/11/174,186

## CURRENT FILING DATE: 2001-05-03

## PRIOR APPLICATION NUMBER: US 60/288,564

## PRIOR PILING DATE: 2001-05-03

## NUMBER OF SEQ ID NOS: 42

## SEQ ID NO 17

## LEMOTH: 116

## US OFTWARE: PATENTIN VERSION 3.3

## LEMOTH: 116

## US OFTWARE: PATENTIN VERSION 3.3

## LEMOTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/11174186

Sequence 18, Application US/11174186

Publication No. US20050244418A1

GENERAL INFORMATION:

APPLICANT: Gillies, Stephen

APPLICANT: Gillies, Stephen

APPLICANT: Gillies, Stephen

APPLICANT: Allies, Stephen

TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

FILE REPERENCE: LEX-019

CURRENT APPLICATION NUMBER: US/11/174,186

CURRENT FILING DATE: 2005-07-01

PRIOR APPLICATION NUMBER: US 60/288,564

PRIOR PILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.3

SEQ ID NO 18
OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
                                                                                                                                                                                                                                                           Gapa
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Pred. No. 0.02;
1; Mismatches 0; Indels
                                                                                                                                                                                                   Length 116;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                Score 55; DB 7;
Pred. No. 0.02;
1; Mismatches
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CTHER INFORMATION: VH7 heavy chain
US-11-174-186-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: VH6 heavy chain US-11-174-186-17
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Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                      1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                                                       26 GYTFINYGMN 35
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ORGANISM: Artificial
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INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ION: (70)... (70)
INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /KEY: misc feature
TION: (80)...(80)
R INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAMENYERY: misc feature
LOCATION: (88)...(88)
OTHER INFORMATION: wherein Xaa at position 88 is an asparagine, an alanine or
OTHER INFORMATION: serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (63)..(63)
OTHER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /KEY: misc_feature
TION: (68)..(68)
R INFORMATION: wherein Xaa at position 68 is a phenylalanine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (91)...(91)
OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (46)..(46)
OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /KEY: misc feature
TION: (83) ... (83)
R INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (84)...(84).
OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEDITORY:
MENE/KEY: misc_feature
LOCATION: (85)...(85)
OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                            ION: (40)...(40)
INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (69)...(69)
OTHER INFORMATION: wherein Xaa at position 69 is an alanine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ION: (76)...(76)
INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
                                                                                                                                                                                                                                   arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
.OCATION: (65)...(65)
OTHER INFORMATION: wherein Xaa at position 65 is a lysine or a glutamine
           OTHER INFORMATION: wherein Kaa at position 11 is a leucine or a valine
                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (38)...(38)
OTHER INFORMATION: wherein Xaa at position 38 is a lysine or an
                                                                                                                      OTHER INFORMATION: wherein Xaa at position 17 is a threonine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
**ACATION: (63)...(63)
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LOCATION: (91)..(91)
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NAME/KEY: misc_feature
LOCATION: (93)...(93)
                                                              NAME/KEY: misc_feature
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LOCATION: (40)...(40)
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LOCATION: (46)..(46)
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TYPE: PRT
ORGANISM: Artificial
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US-11-174-186-23
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US-11-174-186-20

Sequence 20, Application US/11174186

Publication No. US20050244418A1

GENERAL INFORMATION:

APPLICANT: Gillies, Stephen

APPLICANT: Gillies, Stephen

APPLICANT: Gillies, Stephen

TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

FILE REPERENCE: LEX-019

CURRENT FILING DATE: 2005-07-01

PRIOR APPLICATION NUMBER: US 60/288,564

PRIOR PLING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.3

SEQ ID NO 20

LENGTH: 116
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Pred. No. 0.02;
Score 55; DB 7; Length 116;
Pred. No. 0.02;
1; Mismatches 0; Indels
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; OTHER INFORMATION: VH2.5 heavy chain US-11-174-186-19
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     94.8%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
    Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Sequence 22, Application US/11174186

Publication wo. US20050244418A1

Publication wo. US20050244418A1

GENERAL INFORMATION:
APPLICANT: Glilies, Stephen
APPLICANT: Lo, Kin-Ming
CURRENT APPLICANTION NUMBER: US/11/174,186
CURRENT PILING DATE: 2005-07-01
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.3

SEQ ID NO 22

LENGTH: 116
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Sequence 21, Application US/11174186

Publication No. US20050244418A1

GENERAL INFORMATION:
APPLICANT: G1111es, Stephen
APPLICANT: G111es, Stephen
APPLICANT: G111es, Stephen
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
CURRENT PILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR APPLICATION NOS: 42
SOFTWARE: Patentin version 3.3
SEQ ID NO 21
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Pred. No. 0.02;
1; Mismatches 0; Indels
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Pred. No. 0.02;
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; OTHER INFORMATION: KS de-1mmunized VH2
US-11-174-186-22
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US-11-174-186-21
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Search completed: April 25, 2006, 07:10:01 Job time : 7.58176 secs
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US-11-174-186-24
i Sequence 24, Application US/11174186
i Publication No. US20060244418A1
i GENERAL INFORMATION:
i APPLICANT: Qillies, Stephen
i APPLICANT: Qian, Xiugi
i TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
i TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
i FILE REPRENT FILING DATE: 2005-07-01
i PRIOR PILING DATE: 2005-07-01
i PRIOR FILING DATE: 2001-05-03
i NUMBER OF SEQ ID NOS: 42
i SOFTWARE: PatentIn version 3.3
i SEQ ID NO 24
i LENGTH: 116
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US-11-174-186-25
Sequence 25, Application US/11174186
Sequence 25, Application Wo. US20050244418A1
GENERAL INFORMATION:
APPLICANT: G1111es, Stephen
APPLICANT: G1111es, Stephen
APPLICANT: G1111es, Stephen
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Lo, Kin-Ming
APPLICANT: Older, Xiugi
TITLE OF INVENTOW: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT APPLICATION NUMBER: US 60/288,564
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.3
SEQ ID NO 23
LENGTH: 116
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Pred. No. 0.02;
1; Mismatches 0; Indels
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Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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ORGANISM: Artificial
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PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.3
SEQ ID NO 25
LENGTH: 116
                                                                                                                                                                                                                OTHER INFORMATION: KS de-immunized VH5
                                                                                                                                                                                                                                                                                                                                                                                  1 GYTFTNYGIN 10
                                                                                                                                                   TYPE: PRT ORGANISM: Artificial
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Blocceleration Ltd.
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Bw model - protein search, using protein ξ

April 25, 2006, 06:05:16 ; Search time 53.3962 Seconds (without alignments) 82.286 Million cell updates/sec Run on:

US-10-764-428-18 62 1 GYDFTHYGMN 10 score: Sequence: Title: Perfect :

BLOSUM62 Scoring table:

2443163 seqs, 439378781 residues Gapop 10.0 , Gapext 0.5 Searched: 2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

A Geneseq 21:*

1. geneseqp1990s:*

2. geneseqp1990s:*

3. geneseqp2000s:*

5. geneseqp2001s:*

6. geneseqp2003s:*

7. geneseqp2003s:*

9. geneseqp2003s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		•	Abp61231 Anti-VEGF	_		Adf09953 Antibody	•		•	Aaw70682 Anti-VEGF	Aab05900 F(ab)-12		-		Abp61255 Humanised	Abp61257 Humanised	_		Anti-		Aea40494 Anti-VEGF	Abp51953 Plasmid p	Abb81110 Anti-VEGF	Adol4129 Plasmid p
SUMMARIES	£	AAW70662	AAW70698	ABP61231	ABP61267	AD090714	ADF09953	ADF10058	AAW70686	AAW70688	AAW70682	AAB05900	AAB13382	AAB13385	AAB13384	ABP61255	ABP61257	ABP61251	AAB05902	AAB13391	ADG31769	AEA40494	ABP51953	ABB81110	AD014129
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	Length DB	10	10	10	10	10	117	117	118	118	118	118	118	118	118	118	118	118	121	121	123	123	254	476	476
	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62
	Result	1	(4)	(1)	4	LC1	•	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Add90730 Anti-VEGF Add90733 Anti-VEGF Aea40565 Anti-VEGF Aea40553 Anti-VEGF			Aea40573 Anti-VEGF Aea1137 Human INF Aea40548 Anti-VEGF Aea4054 Anti-VEGF	AdczelsB Anti-VEGF AdczelsB Anti-VEGF Adczels Anti-VEGF Adczels Anti-VEGF Aawy0667 Fab-phage Abb61236 Anti-VEGF	
ADQ90730 ADQ90733 AEA40565	AAW70664 AAW70666 ABP61233	ABP61235 AAW70665 ABP61234 AEA40569	AEA40573 AEA17137 AEA40548 AEA40544	ADC26162 ADC26161 ADC26161 ADC26163 AAW70667 ABP61236	
	1000	9 5 5 5 5 5 6 5 6 5 6 5 6 5 6 5 6 5 6 5	10 9 1123 9 123 9	2334 2334 7 234 7 234 7 2 01 7 2 01	•
100.0	រល់ល់ល	93.5 88.7 88.7		888.7 7.2 88.7 7.1 1.1	:
2002	2000	2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	50505	លលលលល លសលស សសសស	5
25 27 27	330 310 310	3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	36 33 38 38	4 4 4 4 4 4 0 11 13 16 18 4 18	,

ALIGNMENTS

AAW70662 ID AAW7

AAW70662 standard; peptide; 10 AA

AAW70662;

27-JAN-1999 (first entry)

Fab-phage library HL-265 anti-VEGF variant Y0243-1.

Murine; humanised antibody; VEGF-induced angiogenesis; tumour; anti-vascular endothelial growth factor antibody; anti-VEGF antibody; retinal disorder; age-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

Synthetic.

WO9845331-A2.

15-0CT-1998

98WO-US006604. 03-APR-1998;

97US-00833504. 97US-00908469. 07-APR-1997; 06-AUG-1997;

(GETH) GENENTECH INC.

Chen YM; Lowman HB, Wells JA, Presta LG, Baca M,

WPI; 1998-568337/48.

New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other anglogenic states, also related nucleic acid, vectors and transformed cells.

Example 3; Page 74; 100pp; English.

(anti-VEGF) antibody variants from Pab-phage library Hi-265. The sequences are used in the course of the invention to produce the humanised anti-VEGF antibody of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. agerelated macular degeneration or diabetic retinal disorders (e.g. agerelated macular degeneration or diabetic retinal disorders (e.g. agereated the conditions that involve angiogenesis, e.g. rheumatoid arthitis, psoriasis, atherosclerosis, Grave's disease, etc

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06-APR-1998;
                                                                                                                                                                                                                                           06-AUG-1997;
                                                                20-SEP-2002
                                                                                                                                                                                                14-MAR-2002
                                                                                                                                                      Synthetic.
                                           ABP61231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP61267;
                                                                                                                                                                                                                                                               (BACA/)
                                                                                                                                                                                                                                                                           (WELL/)
(PRES/)
                                                                                                                                                                                                                                                                                                 (LOWM/)
                                                                                                                                                                                                                                                                                                           (CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP61267
ID
          ABP6123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a heavy chain hypervariable region of the murine anti-vascular endothelial growth factor (anti-VEGF) antibody. The sequence is used to construct the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve anglogenesis, e.g. rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                                                                                                                                         Heavy chain hypervariable region; murine; humanised antibody; anti-vascular endothelial growth factor antibody; anti-VEGF antibody; VEGF-Induced anglogenesis; tumour; retinal disorder; age-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
                                                       Gaps
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                              100.0%; Score 62; DB 2; Length 10; 100.0%; Pred. No. 0.00091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
                                                                                                                                                                                                                      Anti-VEGF antibody heavy chain hypervariable region CDRH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 62; DB 2; Length 10
100.0%; Pred. No. 0.00091;
ive 0; Mismatches 0; Indels
                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen YM;
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lowman HB,
                                                                                                                                                      AAW70698 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 81; 100pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            97US-00833504
97US-00908469
                                                                                                                                                                                                (first entry)
                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100
                                                                           1 GYDFTHYGMN 10
                                                                                        GYDFTHYGMN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-568337/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 AA;
           Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                        03-APR-1998;
                                                                                                                                                                                                                                                                                                                                            WO9845331-A2
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06-AUG-1997;
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                                                                                                                                                                                                                                                                                                            Synthetic.
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                                Query Match
                                                                                                                                                                            AAW70698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baca M,
                                                                                                                                                                                                                                                                                                                      Мив вр.
                                            Best Loc
Matches
                                                                                                                                          AAW70698
ID AAW7
                                                                                                                                RESULT
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The present invention relates to humanised anti-VEGF (vascular endothelial growth factor) antibodies or a variant of a parent anti-VEGF antibody, which binds human VEGF. The anti-VEGF antibodies are useful for inhibiting VEGF-induced angiogenesis in a mammal (particularly a human), particularly those having a tumour or a retinal disorder e.g. intraocular neovascular disorders. The present sequence is a peptide fragment of an anti-VEGF variant from a second generation Fab-phage library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                 Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; angiogenesis inhibitor; tumour; retinal disorder; intraocular neovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; angiogenesis inhibitor; tumour; retinal disorder; intraocular neovascular disorder; heavy chain; variable domain; CDRHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised anti-VEGF antibody heavy chain variable domain, CDRH1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presta LG, Lowman HB, Chen YM;
                                                                                                                                                             Anti-VEGF antibody VH1 peptide Y0243-1.
ABP61231 standard; peptide; 10 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 29; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0054856P
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Best Local Similarity 100.v.
The Conservative
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                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYDFTHYGMN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACA M.
WELLS J A.
PRESTA L G.
LOWMAN H B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-517920/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHEN Y M.
                                                                                                                                                                                                                                                                                                                                                                                        US2002032315-Al.
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Gaps

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GYDFTHYGMN 10 1 GYDFTHYGMN 10

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Matches

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The present invention relates to humanised anti-VEGF (vascular endothelial growth factor) antibodies or a variant of a parent anti-VEGF antibody, which binds human VEGF. The anti-VEGF antibodies are useful for inhibiting VEGF-induced angiogenesis in a mammal (particularly a human), particularly those having a tumour or a retinal disorder e.g. intraocular neovascular disorders. The present sequence is an exemplary heavy chain variable domain of the humanised anti-VEGF antibody of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antianflammatory; antiangiogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; andiogenic disorder; immunological disorder; anti-VRGF antibody; anti vascular endothelial cell growth factor antibody; heavy chain; HVRI.
                                                                                                                                                                                                                                                                                                          New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-VEGF antibody heavy chain HVR1 peptide SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 62; DB 5; Length 10
100.0%; Pred. No. 0.00091;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        Chen YM;
                                                                                                                                                                                                                                                         Lowman HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ90714 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                      Claim 23; Page 31; 47pp; English.
                                                                                                                                                                                                                                                         Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-2004; 2004WO-US001844.
                                                                                                                     98US-00056160
                                                                                                                                                97US-0054856P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYDFTHYGMN 10
                                                                                                                                                                        BACA M.
WELLS J A.
PRESTA L G.
LOWMAN H B.
CHEN Y M.
                                                                                                                                                                                                                                                                                   WPI; 2002-517920/55
                                                                                                                                                                                                                                                         Wells JA,
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nes 10; Conserv
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                                                                US2002032315-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-2004
            Homo sapiens
                                                                                                                      36-APR-1998;
                                                                                                                                                06-AUG-1997;
                                                                                           14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                           Mus sp.
Synthetic.
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                                                                                                                                                                         (BACA/)
(WELL/)
(PRES/)
(LOWM/)
(CHEN/)
                                                                                                                                                                                                                                                         Baca M,
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Matches
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ADQ90714
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Gaps ; 0

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Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework
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                                                                                                                                                                                                                                           100.0%; Score 62; DB 8; Length 10; 100.0%; Pred. No. 0.00091; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        Antibody heavy chain variable region 1CZ8(7-4-1).
                                                                     Claim 13; SEQ ID NO 18; 161pp; English
                                                                                                                                                                                                                                                                                                        ADF09953 standard, protein; 117 AA.
    23-JAN-2003; 2003US-0442484P.
                                                                                                                                                                                                                                                                                                                              12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                  1 GYDFTHYGMN 10
                                                                                                                                                                                                                                                                             1 GYDPTHYGMN 10
                                                          region in a host cell
               (GETH ) GENENTECH INC
                                    WPI; 2004-562149/54.
                                                                                                                                                                                                                                  Sequence 10 AA;
                           Simmons L;
                                                                                                                                                                                                                                                                                                                   ADF09953;
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                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                   ADF09953
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Antibody, stability, solubility, antigen binding affinity; variable region; human.

03-MAR-2003; 2003WO-US006598.

WO2003074679-A2

12-SEP-2003.

ношо варіепв

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physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acid at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody variable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a variable heavy domain of an affinity-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-VEGF humanised antibody variable heavy domain of variant Y0313-1
                                                                                                                       The present invention relates to a method for optimizing at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heavy variable domain; murine; humanised antibody;
anti-vascular endothelial growth factor antibody; anti-VEGF antibo
VEFF-induced anglogenesis; tumour; retinal disorder;
age-related macular degeneration; diabetic retinopathy;
rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
comprises analyzing the interactions of amino acids at variable positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 62; DB 7; Length 117; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen YM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW70686 standard; peptide; 118 AA.
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                                                                          Example 6; Fig 16a; 135pp; English
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97US-00908469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 GYDFTHYGMN 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wells JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9845331-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-1998;
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06-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW70686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                         physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; structure; selecting at least one amino acid to be considered at the variable position the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical property. The method is useful for optimizing solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody may be variable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                          present invention relates to a method for optimizing at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                     Computer optimization of physicochemical properties of antibodies comprises analyzing the interactions of amino acids at variable positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer optimization of physicochemical properties of antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 62; DB 7; Length 117; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                solubility; antigen binding affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                 Dahiyat B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dahiyat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF antibody heavy chain variable region 1CZ8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                 Marshall SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desjarlais JR, Marshall SA,
                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2a; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF10058 standard; protein; 117 AA
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29-MAY-2002; 2002US-0384197P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-2003; 2003WO-US006598.
                                   01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody; stability; solubil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                 Desjarlais JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100 les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYDFTHYGMN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYDFTHYGMN 10
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                                                                                                                                                                                           WPI; 2003-722066/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003074679-A2
                                                                                                       (XENC-) XENCOR
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                                                                                                                                                 Lazar GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lazar GA,
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Matches

RESULT 7

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Gaps

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The present sequence represents a variable heavy domain of an affinity-matured anti-vascular endothelial growth factor (anti-VBGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VBGF antibody of the invention. The humanised anti-VBGF antibody of the invention. The humanised antibodies are used to inhibit VBGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinapathy). They can also be used to treat other conditions that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
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matured anti-vascular endothelial growth factor (anti-VEGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve angiogenesis, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                                                                                                                                    rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heavy variable domain; murine; humanised antibody; anti-VEGF antibody; anti-vascular endothelial growth factor antibody; anti-VEGF antibody; VEGF-induced angiogenesis; tumour; retinal disorder; age-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 62; DB 2; Length 118; 100.0%; Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW70688 standard; peptide; 118 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                               Sequence 118 AA;
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Homo sapiens.
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AAW70688
AAW7068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other anglogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                                                                                                                                                         Anti-VEGF humanised antibody variable heavy domain of variant Y0243-1.
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                                                                                                                                                                                                                                                                                                      anti-VEGF antibody;
                               Gaps
                                                                                                                                                                                                                                                                                Heavy variable domain; murine; humanised antibody; anti-VEGF antibc anti-vascular endothelial growth factor antibody; anti-VEGF antibc VEGF-induced angiogenesis; tumour; retinal disorder; age-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
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100.0%; Score 62; DB 2; Length 118; 100.0%; Pred. No. 0.011; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 10B; 100pp; English
                                                                                                                                                                      AAW70682 standard; peptide; 118 AA.
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97US-00908469
                                                                                                                                                                                                                                 (first entry)
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Matches 10; Conservative
                                    Conservative
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                                                                 1 GYDFTHYGMN
                                                                                            GYDPTHYGMN
                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                     AAW70682;
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      Query Match
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Matches 1
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RESULT 11 AAB05900

Sequence 118 AA;

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Anti-VEGF antibody YO243-1 heavy chain variable domain.
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                                                                                                                                         Unidentified
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Region
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the heavy chain variable domain of the F(ab)-12 antibody variant Y0238-3. F(ab)-12 is a humanised anti-vascular endothalial growth factor (VEGF) antibody. F(ab)-12 was the parent artibody used in the production of a large number of antibody variants containing randomised peptide inserts within the complementarity determining regions (CDRS). Phage display libraries were subjected to eight rounds of selection to isolate variants with an antigen binding affinity at least two-fold stronger than the binding affinity of parent antibody for the target VEGF antibody. The anti-VEGF antibody variants may be useful in diagnostic assays for detecting expression of VEGF in cells, tissue or serum. They may also be used in the prevention and treatment of neoplastic diseases such as breast cancer, lung cancer and arthritis, psoriasis, atherosclerosis, and diabetic and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                            Antibody variants with higher binding affinity than native antibodies useful for diagnosis, prevention and treatment of neoplastic and non-neoplastic diseases comprises amino acid insertion in hypervariable
                                                                                        Humanised; F(ab)-12; heavy chain variable domain; antibody variant; phage display; randomised library; cytostatic; antiarthritic; antipsoriatic; antidiabetic; antiinflammatory; antiarteriosclerotic; vascular endothelial growth factor; VEGF; breast cancer; lung cancer; retinoblastoma; rheumatoid arthritis; psoriasis; atherosclerosis; diabetic retinopathy; complementarity determining region; CDR.
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                                                                     F(ab)-12 antibody variant Y0238-3 heavy chain variable domain.
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100.0%; Pred. No. 0.011;
iive 0; Mismatches 0; Indels
 AAB05900 standard; peptide; 118 AA.
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                                                                                                                                                                                                                                                                                                                                Muller Y;
                                                                                                                                                                                                                                                            99WO-US027153.
                                                                                                                                                                                                                                                                                 98US-0108945P
                                             (first entry)
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                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                              Chen YM, Lowman HB,
                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-387797/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                              WO200029584-A1
                                                                                                                                                                            Homo sapiens.
Synthetic.
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                                              17-0CT-2000
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                       AAB05900;
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The present sequence is the heavy chain variable region of the affinity matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody CC TO (2014)—1. Humanised F(ab)—12 and affinity matured anti-VEGF antibodies may be used to treat conditions characterised by undesirable excessive neovascularisation. Such conditions include tumours (especially solid neovascularisation, such conditions include tumours (especially solid other retinopathies, retrolental fibroplasia, age-related macular degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias (including Grave's disease), corneal and other tissue transplantation, and chronic inflammation. Oedemas associated with malignancies, meig's syndrome, head trauma, and ascites associated with malignancies, meig's syndrome, effusion, may also be traated Monoclonal antibodies are generated in hybridoma cells and those with affinity for VEGF are identified by immunoprecipitation or by an in vitro binding assay
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YO243-1; vascular endothelial cell growth factor; VEGF; antibody; antiinflammatory; cerebroprotective; cytostatic; antifheumatic; antipariatic; antiarteriosclerotic; antidabetic; antithritic; antipariatic; antiarteriosclerotic; antidiabetic; antithrioid; excessive neovascularisation; tumour; rheumatoid arthritis; psoriasis; atherosclerosis; diabetes; retrolental fibroplasia; neovascular glaucoma; haemangioma; thyroid hyperplasia; grave's disease; tissue transplantation; inflammation; oedema; trauma;
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                                                                                                                                                                                                                                                                      complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                         cocation/Qualifiers
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/label= CDR-H2
70. 70
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/label= CDR-H1
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/label= CDR-H3
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/label= CDR-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Bruggen N, Ferrara N;
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AAB13385 standard; protein; 118 AA.

Y0317; vascular endothelial cell growth factor; VEGF; antibody; antilnflammatory; cerebroprotective; cytostatic; anticheumatic; antiarterituc; antisoriatic; antidabetic; antichtic; antisoriatic; antidabetic; antichyroid; excessive neovascularisation; tumour; rheumatoid arthritis; psoriasis; atherosclerosis; diabetes; retrolental fibroplasia; tissue transplantation; inflammation; oedema; trauma; Grave's disease; complementarity determining region; CDR. Anti-VEGF antibody YO317 heavy chain variable domain. Location/Qualifiers 26. .35 /label= CDR-H1 (first entry) 50. .66 /label= WO200037502-A2 22-DEC-1998; Unidentified 09-DEC-1999; 21-NOV-2000 29-JUN-2000 AAB13385 Region Region Region Region ξę

CDR-H2

Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and chronic inflammation in a mammal, comprises administering a human vascular endothelial cell growth factor antagonist. 99. .112 /label= CDR-H3 70. .79 /label= CDR-7 98US-00218481. 99WO-US029475 Van Bruggen N, Ferrara N; (GETH) GENENTECH INC WPI; 2000-442646/38.

The present sequence is the heavy chain variable region of the affinity matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody (YO17). Humanised F(ab)-12 and affinity matured anti-VEGF antibodies may be used to treat conditions characterised by undesirable excessive neovascularisation. Such conditions include tumours (especially solid ones), rheumatoid arthritis, psoriasis, atherosoflerosofls, diabetes and cher retinopathies, retrolental fibroplasia, age-related macular degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasias (including Grave's disease), corneal and other tissue transplantation, and chronic inflammation. Ocdemas associated with tumours, strokes and head trauma, and ascites associated with malignancies, meig's syndrome, lung inflammation, nephroite syndrome, pericadial effusion and pleural effusion and pleural effusion and pleural offusion, may also be treated. Monoclonal antibodies are generated in hybridoma cells and those with affinity for VEGF are identified by immunoprecipitation or by an in vitro binding assay Disclosure; Fig 14B; 60pp; English.

Sequence 118 AA;

Gaps ô 100.0%; Score 62; DB 3; Length 118; 100.0%; Pred. No. 0.011; Live 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 10; Conservative

26 GYDFTHYGMN 35

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AAB13384 standard, protein; 118 RESULT 14 AAB13384

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AAB13384;

(first entry) 21-NOV-2000 Anti-VEGF antibody Y0313-1 heavy chain variable domain.

antiinflammatory; cerebroprotective; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic; antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis; psoriasis; atherosclerosis; diabetes; retrolental fibroplasis; neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease; tissue transplantation; inflammation; oedema; trauma; (0313-1; vascular endothelial cell growth factor; VEGF; antibody;

Location/Qualifiers Region

Unidentified

50. .66 /label= CDR-H2 70. .79 /label= CDR-H1 99. .112 /label= CDR-H3 /label= CDR-7 Region Region Region

WO200037502-A2

29-JUN-2000

99WO-US029475 09-DEC-1999; 98US-00218481 22-DEC-1998;

(GETH) GENENTECH INC

Van Bruggen N, Ferrara

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WPI; 2000-442646/38.

Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and chronic inflammation in a mammal, comprises administering a human vascular endothelial cell growth factor antagonist.

Disclosure, Fig 14B; 60pp; English.

The present sequence is the heavy chain variable region of the affinity matured anti-vascular endothelial cell growth factor (anti-VEGF) antibody constructed anti-vascular endothelial cell growth factor (anti-VEGF) antibody volid to the construction of the construction of the constituent of the co

Sequence 118 AA;

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Query Match

100.0%; Score 62; DB 3; Length 118;

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                                                                                                                                                                                                                 Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; angiogenesis inhibitor; tumour; retinal disorder; intraocular neovascular disorder; Y0313-1; heavy chain; variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
            Gaps
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                                                                                                                                                                                               Humanised anti-VEGF Y0313-1 antibody variable heavy domain.
           Indels
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Pred. No. 0.011;
0; Mismatches 0;
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                                                                                                                        ABP61255 standard; protein; 118 AA.
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/label= CDR-H2
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Best Local Similarity 100.
Matches 10; Conservative
                                                    26 GYDFTHYGMN 35
                                   1 GYDFTHYGMN 10
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WELLS J A.
PRESTA L G.
LOWMAN H B.
CHEN Y M.
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Best Local Similarity
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                                                                                                                                                                       20-SEP-2002
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Synthetic.
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(PRES/)
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ABP61255
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Search completed: April 25, 2006, 06:15:09 Job time : 54.3962 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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protein search, using sw model OM protein April 25, 2006, 06:15:41; Search time 8.49057 Seconds (without alignments) 113.322 Million cell updates/sec Run on:

US-10-764-428-18 62 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 GYDFTHYGMN 10 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	* .	Description	heavy	heavy chai	mAb heavy ch	heavy chain	heavy	chain	heavy	heavy chain V	heavy	heavy chain V	heavy	BHD9D10 protein -	g heavy chain V	heavy chain V	heavy chain V	heavy chain V	g heavy chain V	_	g heavy cha	heavy cha	Ig heavy chain V r								
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dp	Query	Match		77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4		74.2	74.2	74.2	4		4	74.2	72.6	72.6	71.0	67.7	67.7	-	~	2
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ALIGNMENTS

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Cispecies: Mus musculus (house mouse)
Cispecies: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
Cispeciestor: C24672
Cispeciestor: C24672
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Recession: C24672
A;Residues: 1-93 <WIN>
A;Residues: 1-93 <WIN>
A;Residues: 1-93 <WIN>
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin

Length 93,

Gaps ö 1; Indels Query Match 77.4%; Score 48; DB 2; Best Local Similarity 80.0%; Pred. No. 0.18; Matches 8; Conservative 1; Mismatches

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Secists

Substance Strain V region - mouse (fragment)

Gradies: Mus musculus (house mouse)

Gradies: Substance Secists

Ristark, S. B.; Caton, A.J.

J. Exp. Mac. 174, 613-624, 1991

Article: Antibodies that are specific for a single amino acid interchange in a protein e A; Reference number: S26309; MUID:91341421; PMID:1908510

Arcession: S26326

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Gradies: 1-99 < STAA

Gradies: 1-99 < STAA

Gradies: 1-90 < STAA

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Gape ö 77.4%; Score 48; DB 2; Length 99; 80.0%; Pred. No. 0.19; 1; Indels tive 1; Mismatches 1; Indels Query Match Best Local Similarity 80.0 Matches 8; Conservative

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1 GYDPTHYGMN 10 ઠે 셤

GYTFTNYGMN 15

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C;Accession: S26325
R;Stark, S.E.; Caton, A.J.
Bxp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein el A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26325
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C;Cyberfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;S-88/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPARC:UP1000011648E; EMBL:Z15022; NID:G52619; PIDN:CAA78741.1; PID
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S;19968
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Reference number: S;19963
A;Reference number: S;19968
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 31-Dec-2004
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A;Residues: 1-115 <#RI>
A;Cross-references: UNIPROT:Q921A6; UNIPARC:UPI000017696A; EMBL:X65089
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C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                              A,Cross-references: UNIPARC:UPI000011648B; EMBL:Z15013
R;Thomas, J.W.
submitted to the EMBL Data Library, August 1992
A;Reference number: $24776
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                                      A;Molecule type: DNA
A;Residues: 1-105 «KLA»
A;Cross-references: UNIPARC:UP1000011648E; EMBL:Z15001
A;Accession: S24773
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A;Residues: 1-105 <THO>
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A;Residues: 1-109 <STA>
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                                                                        Ig heavy chain V region (VGAM3-8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C;Accession: D24672
K;Winter, B.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Accession: D24672
A;Molecule type: DNA
A;Residues: 1-101 <WIN>
A;Residues: 1-101 <WIN>
A;Coss-references: UNIPARC:UPIO000113758; GB:X03301; NID:951757; PIDN:CAA27040.1; PID:9
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UP1000011648C; EMBL:Z15020; NID:g52616; PIDN:CAA78739.1; PID
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Ig heavy chain V region (subgroup XI) - mouse (fragment)
Ig heavy chain V region (subgroup XI) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Peb-1995 #sequence_revision 21-Nov-1998 #text_change 23-Jul-1999
C;Accession: 824764; 824772; $24777
S;Klages, S
submitted to the EMBL Data Library, August 1992
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C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence revision 21-Nov-1998 #text_change 23-Jul-1999
C;Accession: S24765; S24773; $\overline{S}24778$
R;Klages, S
B;Klages, C
A;Reference number: S24763
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77.4%; Score 48; DB 2; Length 101;
Best Local Similarity 80.0%; Pred. No. 0.2;
Matches 8; Conservative 1; Mismatches 1; Indels
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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A;Reference number: $24763
A;Recession: $24764
A;Rocession: $24764
A;Rocession: $24764
A;Residues: 1-105 < KIDA
A;Residues: 1-105 < KIDA
A;Residues: 1-105 < KIDA
A;Accession: $24772
A;Residues: 1-105 < KIDA
A;Residues: 1-105 < KIDA
A;Residues: 1-105 < KIDA
A;Residues: 1-105 < KIDA
A;Reference number: $24776
A;Reference number: $24776
A;Residues: 1-105 < THO>
A;Residues: 1-105 < THO
A;Residues: 1-105 < THO
A;Residues: 1-105 < THO
A;Residues: 1-105 < THO
A;Residues: 
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Matches 8, Conservative
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A; Cross-references: UNIPARC: UPI000017694C
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A;Molecule type: DNA
A;Residues: 1-124 <SHI>
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C;Species: Mus musculus (house mouse)
C;Date: 06-Peb-1995 #sequence_revision 06-Feb-1995 #text_change 31-Dec-2004
C;Accession: $19965
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: $19963
A;Accession: $19963
A;Actatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 < WREIS
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80.0%; Pred. No. 0.23;
ive 1; Mismatches 1; Indels
                                                                                                       Length 115;
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Pred. No. 0.22;
1; Mismatches 1
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C;Keywords: heterotetramer; immunoglobulin P;10-93/Domain: immunoglobulin homology <IMM>
                                                                                                          77.4%;
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R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary strucand their pH-reactivity profiles.
A;Reference number: A53285; MUID:92017897; PMID:1922102
                                                                                                                                                                                                                                                              A; Modecule type: DNA; protein
A; Residues: 1-119 < <a href="YAND-COURTION COURTION COURTION">A); Residues: 1-119 < <a href="YAND-COURTION COURTION COURTION COURTING">A); Residues: 1-119 < <a href="YAND-COURTING">A); ROBER-CEFERENCES: UNIPARC: UPI00001100A7; GB: D12736; NID: G220595; PIDN: BAA02228.1; PID: A); Note: sequence extracted from NCBI backbone (NCBIN: 63271, NCBIP: 63299)
C; Superfamily: immunoglobulin vegion; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
P; 15-98/Domain: immunoglobulin homology < IMM>
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C; Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
B; Pcll, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo
B; Pcll, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo
A; Piol. Chem. 267, 15552-15558, 1992
A; Reference number: A42848; MUID:92348410; PMID:1639794
A; Accession: B42848
A; Accession: B42848
A; Accession: B42848
A; Residues: 1-120 < PELD
A; Residues: 1-120 < PELD
A; Cross-references: UNIPARC:UPIO000115333; GB:M90690; NID:9195065; PIDN:AAA38146.1; PID:
A; Cross-reference extracted from NCBI backbone (NCBIN:109960, NCBIP:109961)
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C;Species: Mus musculus (house mouse)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: PH1404; PH1406
R;Shrasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; T.J. Bxp. Med. 176, 1209-1214, 1992
A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Reference number: PH1403; MUID:93018837; PMID:1402663
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Pred. No. 0.23;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 2;
Pred. No. 0.23;
1; Mismatches
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Best Local Similarity 80.v.
Best Local Similarity
Conservative
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GYTFTNYGMN 35
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-120 < FE2>
C; Accession: A53285
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833905
19 heavy chain precursor V region - synthetic
C,Species: synthetic
C,Species: synthetic
C;Accession: 833905
C;Accession: 833905
C;Accession: 833905
C;Accession: 833905
A;Title: Chimeric mouse-human IgG1 antibody that can mediate lysis of cancer cells.
A,Reference number: 833905; MUID:87204152; PMID:3106970
A,Residues: 1-146 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14

149021

19 heavy chain V-XI region - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999

A;Riatle: R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.

A;Ritle: Bleven distinct V-H gene families and additional patterns of sequence variation

A;Rieference number: A47624; MUID:90237760; PMID:2110243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UP10000114C7D; EMBL:M16072; NID:g195270; PIDN:AAA38229.1; PI
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A, Status: preliminary; not compared with conceptual translation
A; Status: preliminary;
A; Molecule type: mRNA
A; Residues: 1-79 cHAI>
A; Residues: 1-79 cHAI>
C, Stores-references: UMTPARC: UPI0000114E8E; GB: M27255; NID: 9214301; PIDN: AAA49777.1; PID: C; Superfemily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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A; Accession: PH1406
A; Molecule type: DNA
A; Residues: 115-121 <SH2>
A; Residues: 115-121 <SH2>
A; Cross-references: UNIPARC: UPI000017694C
C; Genetics: 6/1
A; Introns: 16/1
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 35-118/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                        77.4%; Score 48; DB 2; Length 124;
80.0%; Pred. No. 0.24;
tive 1; Mismatches 1; Indels
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Pred. No. 0.34;
0; Mismatches 2; Indels
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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se 8; Conservative
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RESULT 15 S46460 Ig heavy chain V region (YAC-10) - human

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Ricook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Wint Ricook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Wint Nature Genet. 7, 162-168, 1994
A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telomen A;Reference number: S46460; MUID:95004581; PMID:7920635
A;Accession: 846460
A;Status: preliminary
A;Residues: 1-98 <CCO>
                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UP100001165DC; EMBL:227509; NID:9505445; PIDN:CAA81829.1; PIII C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S46460
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Job time : 8.49057 secs
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Best Local Similarity 80.0
Matches 8; Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 25, 2006, 06:05:44; Search time 53.3962 Seconds (without alignments) 132.131 Million cell updates/sec Run on:

US-10-764-428-18 62 1 GYDFTHYGMN 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Qépilo homo sapien	Q921a6 mus musculu			_	entamoeba	-	cv.		cell	_		-		Q70ca8 streptococc			_	-				Q82p16	Q7×198	O4uiz2	_		-	_	Q4uj64 theileria	Q4ucl8 theileria
SUMMAKIBS	ΙΩ	O6PILO HUMAN	Q921A6 MOUSE	OSPOS1_RAT	QSOPUS_ENTHI	QSONY4_ENTHI	Q50V47 ENTHI	Q50SP0_ENTHI		QSONI1 ENTHI	Q840B9_9GAMM	HV03 MOUSE	HV02_MOUSE	QSXXSO GEOKA	Q74LM7_LACJO	Q70CA8 STRTR	Q935T8 STRTR	Q9NOW4 RABIT	Q9NOW6 RABIT	Q6JI92 9EURY	Q752R9 ASHGO	Q5CJA1 CRYHO	QSCXK4 CRYPV	Q82P16 STRAW	Q7XL98 ORYSA	Q4UIZ2 THEAN	Q4UPD6 THEAN	Q4UFL3 THEAN	O4UHHO THEAN	Q4UBI6 THEAN	O4UJ64 THEAN	Q4UCL8_THEAN
	DB	10	N	N	~	~	~	~	N	~	7	-	-	7	~	7	7	N	~	N	~	0	~	N	~	~	~	~	7	~	~	8
	Query Match Length	125	241	475	176	237	238	260	276	348	486	120	140	264	515	562	562	124	124	162	313	447	449	454	853	1417	1668	1931	2123	2364	2732	3096
*	Query Match	74.2	74.2	74.2	69.4	69.4	69.4	69.4	69.4	69.4	69.4	67.7	67.7	67.7	67.7	67.7	67.7	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1
	Score	46	46	46	43	43	43	43	43	43	43	42	42	42	42	42	42	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
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O92008 mus musculu Q8viji mus musculu Q9vbx9 drosophila Q9vbx8 drosophila Q56f03 aeromonas p Q8a7r9 bacteroides Q07929 strongyloce Q8fsk5 corynebacte Q8ntd8 corynebacte Q5kf9 cryptococcu Q5fg cryptococcu Q5fg mus musculu Q5fg cryptococcu Q5fg borrelia bu
Q920BB_MOUSE Q9VBX9_DROME Q9VBX9_DROME Q9VBX9_DROME Q56F03_9CAUD Q8A7R9_BACTN Q8A7R9_BACTN Q8A7R9_COREP Q8NTD8_CORGL Q5HZY6_MOUSE Q55QL6_CRYNE Q51X11_MOUSE Q51X11_MOUSE
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ALIGNMENTS

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Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
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MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;

Stark S.E., Caton A.J.;

Stark S.E., Caton A.J.;

Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally distinct variable regions.";

J. Exp. Med. 174.613.624(1991).

BMBL; U88067; AAB48044.1; -; mRNA.

PIR; $19967; $19967.

PIR; $19968; $19968.

PIR; $19968; $19968.

PIR; $26325; $26325.

PIR; $26325; $26325.

PIR; $26325; $26325.

PIR; $26325; $26325.
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98170165; PubMed=9509426; Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D., Yi K.S., Suh P.G., Ryu S.H., Chung H.K.; Choring and characterization of coNNs encoding VH and VL of a generation of anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain FV molecule (scFv).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                      DB 2; Length 125
                                                               2; Indels
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                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-CRA 79 single chain Fv (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                              241 AA.
                      Score 46; DB 3
Pred. No. 2.5;
0; Mismatches
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QSPQ31;
01-FEB-2005 (TrEMBLrel. 29, Ca
01-FEB-2005 (TrEMBLrel. 29, La
01-FEB-2005 (TrEMBLrel. 29, La
19ha protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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                      74.2%;
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Q921A6;
Ouery Match
Best Local Similarity 80...
Best Acal Similarity 80...
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Matches 8; Conserv
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SEQUENCE
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OUT 0921A6 MO

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DT 01-F
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OS Ratt
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TISSUB-Lung;

MEDLINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilaion D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilaion D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roderzation and initial analysis of more than 15,000 full-length human
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC087057; AAH87057.1; -; mRNA.
GO; GO:0003823; F:antigen binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 475 AA; $2118 MW; EC61093E69A96708 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
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Pred. No. 9.9;
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PubMed=15729342; DOI=10.1038/nature03291;
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ORFWammes=357.t00005;
Entamocea histolytica HW-1:IMSS.
Bukaryota; Entamocebidae; Entamoceba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR03599; IG_C1.
InterPro; IPR003506; IG_MHC.
InterPro; IPR003596; IG_V.
Pfam; PR07654; C1-set; 2.
SWART; SM00409; IG; 3.
SWART; SM00406; IGC1; 3.
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OT 13-SEP-2005 (TrEWBLrel. 31,

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DT 13-SEP-2005 (TrEMBLrel. 31,

DT 13-SEP-2005 (TrEMBLrel. 31,

DE HYDCHCHICAL PROCLEIN.

GN ORFNAMES-37, L00005,

ENTAMOSDA histolytica HM-11:

OC ENKARYOCA, ENTAMOSDIAGE, ENI

OX NCBL TAXID-294381;

RN LOFTUR SEQUENCE.

RC STRAIN-HM-1.IMS;

RX PUDMEG-15729342; DOI=10.103;

RA LOFTUR B., ANGERSON I., DAV.
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                                                                                                                                                     NUCLEOTIDE SEQUENCE.
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PRT;

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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein.
ORFNames=196.t00002;
                        OSOV47 ENTHI PRELIMINARY;
                                          Q50V47;
               250V47
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PubMed=15729342; DOI=10.1038/nature03291;

PubMed=15729342; DOI=10.1038/nature03291;

PubMed=15729342; DOI=10.1038/nature03291;

A medeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,

A medeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,

B. Hofer M., Buchhaus I., Willhoeft U., Bhatracharya A.,

Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,

Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

Chillingworth T., Churcher C., Stroup S.B., Bhatracharya S., Lohla A.,

Guillen N., Gilchrist C., Stroup S.B., Bhatracharya S., Lohla A.,

Roster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,

R. Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,

Rraser C.M., Hall N.;

R. The genome of the protist parasite Entamoeba histolytica.";

Nature 433:865-868(2005).
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Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T. Suh B., Pop M., Duchene M., Ackers J., Tannich B., Leippe M., Hofer M., Bruchhaus I., Wilhoeft U., Bhattacharya A., Leippe M., Jagels M., Bruchhaus I., Wilhoeft U., Bhattacharya A., Tanniamovorth T., Churcher C., Harris B., Harris D., Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S. Quail M.A., Rabbinowitsch E., Norbertczak H., Price C., Wang Z., Guillen N., Gilchritz-Ponten T., Weber C., Singh U., Mukherjee C., Bl-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B., Fraser C.M., Hall N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1-CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                               "The genome of the protist parasite Entamoeba histolytica.";
Nature 433:865-868(2005).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                              Score 43; DB 2; Length 176; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                               2; Indels
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SEGUENCE 237 AA, 27296 MW; CCE644C6F61A51E1 CRC64;
                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 176 AA; 20448 MW; 916PBEE8A5F67B8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                    preliminary data.
EMBL; AAFB01000926; EAL43614.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
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13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
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ORFNames=407.t00002;
Entamoeba histolytica HM-1:IMSS.
Entamoeba histolytica HM-1:IMSS.
Bukaryota; Entamoebidae; Entamoeba.
NCBI TaxID=294381;
                                                                                                                                                                                                                                                                                                                69.4%;
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Best Local Similarity 70.v.
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Q50NY4 ENTHI PRELIMINARY;
Q50NY4;
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Matches 7; Conservative
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1 GYDFTHYGMN 10 GYDYTGYGRN 89

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STRAIN-HINES,
PubMed=15729342; DOI=10.1038/nature03291;
PubMed=15729342; DOI=10.1038/nature03291;
Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
Amedeo P., Ronchene M., Ackers J., Tarnich B., Leippe M.,
Andeco P., Bruchhaus I., Willhoeft U., Bhattacharpa R.,
Angels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
Angels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
Angels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
Angels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
Angels K., Moule S., Rubost E., Bhattacharpa R.,
Allohist C., Strong S.E., Bhattacharpa R.,
Angels K., Mull N., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
Praser C.M., Hall N.;
R.The genome of the protist parasite Bntamoeba histolytica.";
Nature 433:865-868(2005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEGUENCE 238 AA; 27499 MW; 4354BED1DA574954 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
EMBL; AAFB01000602; EAL45460.1; -; Genomic_DNA.
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Entamoeba histolytica HM-1: IMSS.
Bukaryota, Entamoebidae, Entamoeba.
NCBI TaxID=294381;
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Eukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=294381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
ORFNames=253.t00018, 8.t00068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q50SP0 ENTHI PRELIMINARY;
Q50SP0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 70.0 tes 7; Conservative
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                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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Matches
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STRAIN-HW-1:INSS;

X. PubMed-a15729342; DoI=10.1038/nature03291;
X. PubMed-a15729342; DoI=10.1038/nature03291;
X. Amedea D., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
And B., Pop M., Duchene M., Ackers J., Tannich B., Leippe M.,
And T., Burchaus I., Willhoeft U., Bhattacharya A.,
And T., Churcher C., Hance Z., Harris B., Harris D.,
And Hofer M., Rabbinowitsch B., Norbertczak H., Price C., Wang Z.,
Guillen N., Glichrist C., Stroup S.R., Bhattacharya S., Lohia A.,
Roster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RI-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
The genome of the protist parasite Entamoeba histolytica.";
Nature 433:865-868(2005).

EMBL/Genbank/DBBJ whole genome shotgun (WGS) entry which is
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Biochem. J. 371:1027-1043 (2003).

EMBL, AXI87034; AA031762.1; -; Genomic DNA.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl ...

GO; GO:0016985; F:mannan endo-1.4-beta-mannosidase activity; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

GO; GO:0006080; P:mannan metabolism; IEA.

InterPro; IPR002883; Dockerin_CBD_5.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Cellvibrio.
MCBI_TaxID=155077;
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InterPro; IPR003089; AB hydrolase.
InterPro; IPR007033; IAR Tp.
InterPro; IPR000379; Ser_estrs.
PRINTS; PR0011; ABHYDROLASE.
Hydrolase; Hypothetical protein.
SEQUENCE 348 AA; 39832 NW; 6482585020803E85 CRC64;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLRel. 31, Last an
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01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Endo-bl,4-mannanase 26B.
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Q840B9;
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Best Local Similarity 70.0
Matches 7; Conservative
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19 GYDYTGYGRN 28
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TRAIN-EM-1:INSS;

The pubmed-15723342; DoI=10.1038/nature03291;

The pubmed-15723342; DoI=10.1038/nature03291;

Toftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J., Nozaki T., Andeles B., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T., Sth B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M., Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A., Eabprowth T., Churcher C., Hance Z., Harris B., Harris D., Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S., Andell M., Glichrist C., Stroup S.E., Bhattacharya S., Lohia A., Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C., El-sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B., The genome of the protist parasite Entamoeba histolytica.";

Nature 433:865-868(2005).

EMBL/Genbank/DebBJ whole genome shotgun (WGS) entry which is
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            Nature 433:865-868(2005).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.4%; Score 43; DB 2; Length 260; 70.0%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                         EMBL; AAFB01000720; EAL44622.1; -; Genomic DNA.
EMBL; AAFB01000042; EAL51409.1; -; Genomic_DNA.
InterPro; IPR008262; Lipase_AS.
InterPro; IPR00379; Ser_estra
PROSTTE; PS00120; LiPASE_SER; UNKNOWN_1.
Hydrolase; Hypothetical Protein.
SEQUENCE 260 AA; 29344 MW; 5D5298790487EC84 CRC64;
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SEQUENCE 276 AA; 31441 MW; 285F6277B5ED0942 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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InterPro; IRRO03089; AB hydrolase.
InterPro; IRRO03099; Ser estrs.
InterPro; RO0111; ABHYDROLASE.
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ORFNames=240,100009;
Entamoeba histolytica HM-1:IMSS.
Bukaryota; Entamoebidae; Entamoeba.
NCBI_TaxID=294381;
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QSONI1 ENTHI
ID QSONI1 ENTHI PRELIMINARY;
AC QSONI1;
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Best Local Similarity 70.0°
7; Conservative
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Matches 7; Conservative
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87 GYDYTGYGRN 96
                                                                                                                                            preliminary data
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1 GYDFTHYGMN 10
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SEQUENCE
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-I. MISCRILANEOUS: From analysis of the sizes of several other differentiated genes that hybridize to this one, the authors conclude that all of these V regions have rearranged to the same J segment, JH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-83331846; PubMed=6186498; Siekevitz M., Gefter M.L., Brodeur P., Riblet R., Marshak-Rothstein A.; Marshak-Rothstein A.; "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse."; Bur. J. Immunol. 12:1023-1032(1982).
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                         Gaps
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                                                                                                                                     69.4%; Score 43; DB 2; Length 486; 77.8%; Pred. No. 36; 1; Indels :ive 1; Mismatches 1; Indels
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                                                                                              486 AA; 53233 MW; 0494751306D5DD70 CRC64;
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PROSITE; PS50835; IG LIKE; 1.
3D-structure; Hybridoma; Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Last sequence update) 13-SBP-2005 (Rel. 48, Last annotation update) Ig heavy chain V region 36-65.
                                                                                                                                                                                                                                                                                                                                                                                                            120 AA
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Ensembl; ENSMUSGO0000021155; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_V.
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  InterPro; IPR000805; Glyco_hydro_26.
Pfam; PP02013; CBM 10; 1.
Pfam; PP02156; Glyco hydro 26; 1.
PRINTS; PR00739; GLHYDRIASE26.
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                                                                                                                                          Query Match 69.4
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                        198 GYDFMNYGM 206
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Matches 7; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                          HV03 MOUSE
P01747;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
8porulation specific Nacetylmuramoyl-L-alanine amidase (Spore cortex-lytic enzyme) (EC 3.5.1.28).
OrderedLocusNames=GK2231;
                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J00493; AAA38128.1; -; mRNA.
HSSP; P01747; 1JFQ.
SMR; P01746; 20-146
InterPro; IPR00710; Ig-like.
InterPro; IPR003596; Ig_v.
SMRIX; SM04066; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Capra J.D.;
"Somatic mutation in genes for the variable portion of the immunosolbulin heavy chain.";
Science 216:309-311(1982).
-!-SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sime J., Rabbitts T.H., Bstess P., Slaughter C., Tucker P.W., Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geobacillus kaustophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 1; Length 140;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region 93G7 Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                      21-UU-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                            140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 15;
1; Mismatches
                                                                                                                                                                                                                         Ig heavy chain V region 93G7 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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OSKKSO GEOKA PRELIMINARY;
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                                                                                                               STANDARD;
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GYTPTSYGIN 34
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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055KX50
065KX50
075KX50
075KX50
01-PE
DT 01-PE
DT 01-PE
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102 GYHYTHFGSN 111
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                                                                                                                    RESULT 15
Q70CA8_STR
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                EXECUTION 1970 | 1. STATEMENT | 1. S
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A Pridmore R.D., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
A Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
A Mollet B., Mercenter A., Klaenhammer T., Arigoni F., Schell M.A.;
RT Ameganeme sequence of the probletic intestinal bacterium
Lactobacillus johnsonii NCC 533.";
Lactobacillus johnsonii NCC 533.";
Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
REMBL, RAD12001, AAS08138.1; -; Genomic DNA.
GO; GO:0003796; F:lysozyme activity; IEA.
R GO; GO:000523; P:peptidoglycan catabolism; IEA.
R GO; GO:000523; P:peptidoglycan catabolism; IEA.
R InterPro; IPR002053; Glyco.hydro_25.
R InterPro; IPR003646; SH3_bac.
R InterPro; IPR003646; SH3_bac.
R Fam; PP01083; Glyco.hydro_25; 1.
R SMART; SM00261; Glyco.hydro_25; 1.
R SMART; SM00261; SH3_bac.
R SMART; RM0261; SH3_bac.
R SMART; SM00261; SH3_bac.
R SMART; SM00261; SH3_bac.
R SMART; SM00261; SH3_bac.
R SMART; RM0261; SH3_bac.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.7%; Score 42; DB 2; Length 515; Best Local Similarity 60.0%; Pred. No. 57; Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactobacillus johnsonii.
Bacteria, Frmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00953; GLYCOSYL HYDROL F25; UNKNOWN 1.
Complete proteome; Hypothetical protein.
SEQUENCE 515 AA; 55968 MW; 0D08FB65591ACD04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 AA; 29204 MW; 70EDSF2B46051811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q74LM7_LACJO PRELIMINARY; PRT; 515 AA.

Q774LM7;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Mycothetical protein.
17, Last annotation update)
OrderedLocusNames=LJ0156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLBOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN-NCC 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=14983040; DOI=10.1073/pnas.0307327101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 87.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 GNDFTHYG 117
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1 GYDFTHYGMN 10

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RESULT 15

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PRELIMINARY; PRT; 562 AA.

D 070CAS STRTER

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D 05-UU-2004 (TERMBLEE] 27, Last sequence update)

DT 05-UU-2004 (TERMBLEE] 27, Last sequence update)

DT 05-UU-2004 (TERMBLEE] 27, Last sequence update)

DT 05-UU-2004 (TERMBLEE] 27, Last annotation update)

OS STREPCOCCCUS TREMPLEED 27, Last annotation update)

OS STREPCOCCCUS TREMPLEED 27, Last annotation update)

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ON CRITTAIN-CHRZASS AN CRITTAIN S. (Subsection of Streptococcus transphilus.

ON STAIN-CHRZASS AN CARZASS AN CARZASS
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April 25, 2006, 06:25:05; Search time 13.4906 Seconds (without alignments) 61.284 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                            572060 segs, 82675679 residues
                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                         US-10-764-428-18
62
                                                                                                                                                                                                                            1 GYDFTHYGMN 10
                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                     Scoring table:
                                                                              OM protein
                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/RECOMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RECOMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RECOMB.pep:*

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

SUMMARIES

		*				
Result No.	Score	Query Match	Length	DB	a a	Description
1	62	100.0	10	2	US-08-908-469-86	Sequence 86, Appl
8	62	100.0	10	~	US-08-908-469-128	Sequence 128, App
e	62	100.0		~	US-09-440-781-97	97,
4	62	100.0	118	~	US-08-908-469-112	112,
'n	62	100.0	118	~	US-08-908-469-116	116,
9	62	100.0		~	US-08-908-469-118	118,
7	62	100.0		~	US-09-440-781-99	99, 7
60	28	93.5		~	US-08-908-469-88	88
9	28	93.5	10	~	US-08-908-469-90	90
10	55	88.7	10	~	US-08-908-469-89	89,
11	54	87.1	10	~	US-08-908-469-91	91,
12	52	83.9	10	~	US-08-908-469-87	87,
13	51	82.3	10	~	US-09-440-781-19	5
14	49	79.0	160	~	US-09-318-786-35	m
15	48	77.4		~	US-09-440-781-20	20
16	48	77.4		7	US-08-908-469-1	٦,
17	48	77.4	92	N	US-08-783-853A-84	
18	48	77.4	92	~	US-09-344-050-84	84
19	48	77.4	112	~	US-08-783-853A-20	50, 20,
20	48	77.4		~	US-09-344-050-20	20, A
21	48	77.4		н	US-08-425-336-124	124,
22	48	77.4		Н	US-08-425-336-126	Š
23	48	77.4		-	US-08-488-113B-124	124,
24	48	77.4		-	US-08-488-113B-126	126,
25	48	77.4		Н	US-08-477-484B-124	124,
56	48	77.4		Н	US-08-477-484B-126	126,
27	48	77.4		-	US-08-107-669D-28	Sequence 28, Appl

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Gaps ö

Query Match
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels

Sequence 59, Appl Sequence 66, Appl Sequence 28, Appl Sequence 29, Appl Sequence 89, Appl Sequence 89, Appl Sequence 29, Appl Sequence 67, Appl Sequence 67, Appl Sequence 124, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 89, Appl Sequence 89, Appl Sequence 89, Appl Sequence 89, Appl Sequence 89, Appl		
77.4 118 1 US-08-107-669D-67 77.4 118 1 US-08-107-669D-67 77.4 118 1 US-08-107-669D-67 77.4 118 1 US-08-472-788A-28 77.4 118 1 US-08-472-788A-89 77.4 118 1 US-08-472-788A-89 77.4 118 1 US-08-477-531B-29 77.4 118 1 US-08-477-531B-29 77.4 118 1 US-08-477-531B-29 77.4 118 1 US-08-477-531B-67 77.4 118 1 US-08-477-531B-67 77.4 118 1 US-08-646-360-124 77.4 118 1 US-08-646-360-124 77.4 118 1 US-08-646-360-124 77.4 118 1 US-08-082-842A-29 77.4 118 1 US-08-082-842A-89 77.4 118 1 US-08-082-842A-89 77.4 118 2 US-08-082-842A-89	ALIGNMENTS SULT 1 -08-908-469-86 Sequence 86, Application US/08908469 Patent No. 68844710N: APPLICANT: Baca, Manuel Wells, James A. Presta, Leonard G. Lowman, Henry B. Chem, Yvonne M. TITLE OF INVENTION: ANTI-VEGF ANTIBODIES NUMBER OF SEQUENCES: 131 CORESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc. STREET: 1DAM WAY CITY: South San Francisco STATE: California COMPUTER: California COMPUTER: BADABLE FORM: MEDIUM TYPES: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/908,469 FILING DATE: 21-May-2001 CLASSIFICATION NUMBER: 08/833,504 FILING DATE: 10-May-2001 CLASSIFICATION NUMBER: 08/833,504 FILING DATE: 07-APR-1997 ATTORNEY/AGENT INFORMATION: NAME: Cul. Steven. REGISTRATION NUMBER: 08/833,504 FILING DATE: 07-APR-1997 ATTORNEY/AGENT INFORMATION: NAME: Cul. Steven. REGISTRATION NUMBER: 08/833,504 FILING DATE: 07-APR-1997 ATTORNEY/AGENT INFORMATION: NUMBER: 05/022-9881 INFORMATION FOR SEQ ID NO: 86: SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids TYPER: AMINO ACID ACID TYPER: AMINO ACID ACID TYPER: AMINO ACID TY	000
	POF	4. 0
0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RESOULT Sequ.	806-80-S0

Gaps

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Indels

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) ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-118
; OTHER INFORMATION: humanized antibody heavy chain variable domain
US-09-440-781-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 62; DB 2; Length 118; 100.0%; Pred. No. 0.0055; Live 0; Mismatches 0; Indels
                                                                                                                                                               100.0%; Score 62; DB 2; Length 118 100.0%; Pred. No. 0.0055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITTY: South San Francisco
STATE: California
COUNTRY: USA
ZIF: 94080
ZIF: 94080
ZIF: 94080
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/08/908,469
FILING DATE: 21-May-2001
CILASSIFICATION: cUnknown-
PRIOR APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: CUI, SEEVEN X.
REFERENCE/DOCKET NUMBER: 44,637
REFERENCE/DOCKET NUMBER: 91093P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
                                                                                                                                                                                                           0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-08-908-469-112
; Sequence 112, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Relis, James A. Wells, James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1 DNA Way
                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                     1 GYDFTHYGMN 10
                                                                                                                                                                                                                                                                           26 GYDFTHYGMN 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 11M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                       APPLICANT: Baca, Manuel
Presta, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REGISTRATION NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 128:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yvonne Man-yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 97
                                                                                                                                             Sequence 128, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97, Application US/09440781 Patent No. 6632926 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
GYDFTHYGMN 10
                      GYDPTHYGMN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                           US-08-908-469-128
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LOCATION: 1-121
OTHER INFORMATION: humanized antibody heavy chain variable domain
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARRS: Windatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-MAY-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY ABENT INFORMATION:
NAME: Cul. Steven X.
REGISTRATION NUMBER: 44,637
REGISTRATION NUMBER: P1093P1
TELERPAN: 650/952-9881
TELERPAN: 650/952-9881
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 118:
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Fatent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-yee Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear;
SEQUENCE DESCRIPTION: SEQ ID NO: 118:
US-08-908-469-118
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US-08-908-469-88
Sequence 88, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Mells, James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: TEADABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Geneticch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-MAy-2001
CLASSIFICATION: CURCHOWN:
PRIOR APPLICATION NUMBER: US/08/908,469
FILING DATE: 0.7-APP-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 44,637
REGISTRATION NUMBER: 44,637
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
TEMPSTATION 118 amino acide
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Patent No. 6884879
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                            US-08-908-469-116
; Sequence 116. Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Presta, Leonard G.
; Lownan, Presta, Leonard G.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 118 amino acids
TYPE: Amino Acid
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Best Local Similarity
Matches 10; Conservi
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Score 58; DB 2; Length 10;
Pred. No. 0.0019;
1; Mismatches 0; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRIT APPLICATION NUMBER: US/08/908,469 FILING DATE: 21-May-2001 CLASSIFICATION: CURKNOW>>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 89, Application US/08908469
Patent No. 6684879
GENERAL INFORMATION:
GENERAL INFORMATION:
Mells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFEICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REPERRANCE/DOCKET NUMBER: P1093P1
TELESCOMMUNICATION INFORMATION:
TELEPHONE: 650/225-861
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 aming acids
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APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: CUI, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 560/252-9891
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 antho acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 90:
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.5%;
                                                                                                                                                                                                                                                                                                                                                             TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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90.0%; Pred. No. 0.0019;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER. READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
PRILOR DATE: 21-MAY-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
TILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 44,637
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/952-9674
TELEFAX: 650/952-9674
TELEFAX: 650/952-9674
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Sequence 90, Application US/08908469

Patent No. 6884879

GENERAL INFORMATION:

GENERAL INFORMATION:

Wells, James A.

Presta, Leonard G.

Lowman, Henry B.

COMPANIER OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

STREET: 1 DNA WAY
                                   Lownan, Henry B.

TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: CALL SOUTH SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | LENGTH: 10 amino acids | TYPE: Amino Acid | TYPE: Amino Acid | TYPE: TOPOLOGY: Linear | SEQUENCE DESCRIPTION: SEQ ID NO: 88: US-08-908-469-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
                    Presta, Leonard G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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Query Match

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Pred. No. 0.026;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10;
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                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 2;
Pred. No. 0.018;
1; Mismatches
                                         Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09440781
Sequence 19, Application US/09440781
PAPLICANT: Youne Man-yee Chen et al.
APPLICANT: Youne Man-yee Chen et al.
TILE OF INVENTION: ANTIBODY VARIANTS
FILE REPERENCE: P1469R1
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 19
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIPICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPERENCE/DOCKET NUMBER: P1093P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-08-908-469-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: artificial LOCATION: 1-10 ; COTHER INFORMATION: variant CDR sequence US-09-440-781-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
                                                                                                                               ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                   CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 87:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 83.9
Best Local Similarity 80.0
Matches 8; Conservative
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Pred, No. 0.0084;
                                                            Score 55; DB 2; Length 10;
Pred. No. 0.0058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0, Indels
                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                            APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: «UNLOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 44,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEPAX: 650/952-9891
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-08-908-469-91
       SEQUENCE DESCRIPTION: SEQ ID NO: 89:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 87, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
                                                                                                                                                                                                                            RESULT 11
US-08-908-469-91
; Sequence 91, Application US/08908469
; Patent No. 6884879
; FREENT INFORMATION:
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80.0%;
                                                              88.7%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 87.1
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                           1 GYDFTHYGMN 10
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US-08-908-469-87
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US-08-908-469-89
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                                                                                                                 US-09-318-786-35

Sequence 35, Application US/09318786

Patent No. 6472147

GENERAL INFORMATION:

APPLICANT: Janda, Kim D

APPLICANT: Wirsching, Peter

APPLICANT: Wirsching, Peter

APPLICANT: Lerner, Richard A

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: PILAMENTOUS PHAGE USING PVII AND DIX, COMPOSITIONS,

TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES

FILE REFERENCE: TSR0305S

CURRENT APPLICATION NUMBER: US/09/318,786

CURRENT APPLICATION NUMBER: US/09/318,786

CURRENT FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 35

LENTH: 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: fusion OTHER INFORMATION: polypeptide US-09-318-786-35
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79.0%; Score 49; DB 2; Length 160;
Best Local Similarity 80.0%; Pred. No. 0.97;
Matches 8; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-003-440-781-20

Sequence 20, Application US/09440781

PATENT NO. 6832926

GENERAL INFORMATION:

APPLICANT: Yvonne Man-yee Chen et al.

TITLE OF INYENTION: ANTIBODY VARIANTS

FILE REFERENCE: P146R1

CURRENT APPLICATION NUMBER: US/09/440,781

CURRENT FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 99

SEQ ID NO 20

LENGTH: 10
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; LOCATION: 1-10
; OTHER INFORMATION: variant CDR sequence
US-09-440-781-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: April 25, 2006, 06:28:40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: artificial sequence
1 GYDFTHYGMN 10
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1 GYDFTNYGIN 10
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April 25, 2006, 06:58:17; Search time 43.5849 Seconds (without alignments) 95.866 Million cell updates/sec
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                            1867569 seqs, 417829326 residues
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                       US-10-764-428-18
62
                                                                                                                                                                                                                                1 GYDFTHYGMN 10
                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                     Run on:
                                                                                                                                                                                               Title:
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Published Applications AA Main:*

'cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

'cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000 **Database** :

Total number of hits satisfying chosen parameters:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 86, Appl Sequence 128, App Sequence 86, Appl Description Sequence 1 Sequence 8 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence Sequence Sequence Sequence Sequence 1 Sequence 1 Sequence 5 Sequence Sequence Sequence S Sequence Sequence US-09-056-160B-86 US-09-056-160B-128 US-10-234-671-86 US-10-74-428-18 US-10-974-591-86 US-10-974-591-86 US-10-974-591-86 US-10-379-392-122 US-10-379-392-122 US-10-379-392-124 US-10-379-392-130 US-09-056-160B-112 US-09-056-160B-116 US-09-056-160B-116 US-10-234-671-110 US-10-234-671-110 US-10-234-671-110 US-10-683-043-13 US-10-683-043-13 US-10-683-043-13 US-10-683-043-13 US-10-683-043-13 US-10-683-043-13 Length DB Query Match Score No No Result

۳, د	Sequence 3, Appli	Sequence 56, Appl	Sequence 136, App	Sequence 138, App	Sequence 140, App	Sequence 148, App	Sequence 11, Appl	Sequence 9, Appli	Sequence 11, Appl	Sequence 7, Appli	Sequence 13, Appl	Sequence 127, App	Sequence 95, Appl	Seguence 88, Appl	Sequence 90, Appl	Sequence 88, Appl	Sequence 90, Appl	
US-10-153-176-3	US-10-443-134A-3	US-10-723-434-56	US-10-379-392-136	US-10-379-392-138	US-10-379-392-140	US-10-379-392-148	US-10-020-786-11	US-10-697-995-9	US-11-071-291-11	US-10-764-428-7	US-10-764-428-13	US-10-723-434-127	US-10-723-434-95	US-09-056-160B-88	US-09-056-160B-90	US-10-234-671-88	US-10-234-671-90	
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123	123	123	224	224	224	224	476	476	476	667	667	10	123	10	10	10	10	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	95.2	95.2	93.5	93.5	93.5	93.5	
62	62	62	62	62	62	62	62	62	62	62	62	59	53	28	28	28	28	
28	29	30	31	32	CT	9.6	35	36	37	88	36	40	41	24	4.4	44	45	

ALIGNMENTS

1 GYDFTHYGMN 10

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Sequence 1 Sequence 1 Sequence 2 Sequence 3 Sequence 3

Query Match
100.0%; Score 62; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels

Gaps ö

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CITY: South San Francisco
STATE: California
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
CORPUTER: IBM PC compatible
OPERATING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELEPHONE: 650/225-1896
TELEPHONE: 650/225-1896
INFORMATION FOR SEQ ID NO: 128:
SEQUENCE CHARACTERISTICS:
                                               Josephson 128 Application US/09056160B
| Sequence 128, Application US/09056160B
| Patent No. US20020032315A1
| GENERAL INPORMATION:
| APPLICANT: Baca, Manuel APPLICANT: Wells, James A. APPLICANT: Lowman, Henry B. APPLICANT: Chen, Yoonne M. TITLE OF INVENTION: ANTI-VEGF ANTIBODIES NUMBER OF SECUENCES: 131
| CORRESPONDENCE ADDRESS: ADDRESSES: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California
| CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
STREEF: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 amino acids
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Best Local Similarity 100.
1 GYDFTHYGMN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-056-160B-128
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Gaps
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COMPUTER TEALDANDE TO THE STATE TH
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 135 inch, 1.04 Mb floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03.5ep-2002
CLASSIFICATION: <unknown>PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 125. Application US/10234671

Publication No. US20030190317A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel

Wells, James A.

Presta, Leonard G.

Lowman, Henry B.

Chen, Yvonne M.

TITLE OF INVENTION: AWII-VEGF ANTIBODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 44,637
REFERENCE/POCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELERPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 86: US-10-234-671-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 86:
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TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-974-591-126
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Sequence 18 Application No. US20040229310A1

GENERAL INFORMATION:
APPLICANT: Simmons, Laura
TITLE OF INVENTION: WETHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING
TITLE OF INVENTION: VIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL
TITLE OF INVENTION: CULTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 62; DB 4; Length 10; 100.0%; Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 62; DB 5; Length 10
100.0%; Pred. No. 0.0016; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: YO117 VH HVR1 residues 26-35 US-10-764-428-18
       APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cul., Steven X.
REGISTRATION NUMBER: 44,637
REGISTRATION NUMBER: 91093R2C1
TELECOMMUNICATION OF 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-10-234-671-126
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SAPPLICANT: Baca, Manuel Wells, James A. Presta, Leonard G. Lowman, Henry B. Chen, Yvonne M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYDFTHYGMN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GYDFTHYGMN 10
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US-10-974-591-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-10-764-428-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: BENEVER: PC-COMPUTER: DE-COMPUTER: MINIPARI: MINIPARI: MINIPARI: MINIPARI: MINIPARI: MINIPARI: Genentech)
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Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P1093PlD1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/974,591
PILING DATE: 26-Oct-2004
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/723752
FILING DATE: 27-NOV-2000
APPLICATION NUMBER: 08/908469
FILING DATE: 06-A0C-1997
APPLICATION NUMBER: 08/933504
FILING DATE: 07-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 126, Application US/10974591
Publication No. USZO050112126A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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1 GYDFTHYGMN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 62; DB 5; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0016; Matches 10; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/974,591
FILING DATE: 26-Oct-2004
CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/723752
FILING DATE: 27-NOV-2000
APPLICATION NUMBER: 09/90469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/833504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56, Application US/10379392
Publication No. US20040110226A1
GENERAL INPORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Marshall, Shanton Allcia
CURRENT PAPLICATION UNDHER: US/10/379,392
CURRENT RELING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR PILING DATE: 2002-03-01
SPRIOR PILING DATE: 2002-03-01
PRIOR PILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
TOPOLOGY: Linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-10-974-591-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650/225-8674
TELEPAX: 650/952-981
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Humanized US-10-379-392-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYDFTHYGMN 10
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RESULT 9 US-10-379-392-122

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| Sequence 12, Application (M. 1919)2
| Sequence 12, Application (M. 1919)2
| Publication (M. 1920)4011022641
| GREEAL INFORMATION:
| APPLICANT: Despiration: Application (M. 1916)
| TITLE OF INFORMATION: APPLICANT (M. 1916)
| PRIOR APPLICATION NUMBER: 105 (0.)340,137
| PRIOR PRIVATE PREDENT (M. 105 (M. 1944)137
| PRIOR PRIVATE PREDENT (M. 100 (M. 1944)137
| PRIOR PRIVATE PREDENT (M. 100 (M. 1944)137
| PRIOR PRIVATE PRIVATION (M. 100 (M. 1944)137
| PRIOR PRIVATION (M. 100 (M. 1944)137
| PRIOR PRIVATION NUMBER: 105 (0.)340,137
| PRIOR PRIVATI
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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            100.0%; Score 62; DB 3; Length 118; 100.0%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 35. inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Withbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION DATA:
APPLICATION WHEBR: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 29,616
RESTRENCE/DOCKET NUMBER: 29,616
RESTRENCE/DOCKET NUMBER: 29,616
RESTRENCE/DOCKET NUMBER: 20,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 116, Application US/09056160B

Sequence 116, Application US/09056160B

Patent No. US20020032315A1

GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Fresta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TILLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCES ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                  REGISTRATION NUMBER: 28,616
REPERENCE/POCKET NUMBER: P109:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEPRAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genenced, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: 650/552-9881
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      LENGTH: 118 amino acida
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
NAME: Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYDFTHYGMN 10
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                                                                                                                                                                                                                                                                 US-09-056-160B-112
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LOCATION: (95)...(95)

CTHER INFORMATION: Xaa at position 95 can be Phe, Tyr or Met US-10-379-392-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 62; DB 4; Length 117; 100.0%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRATURE:
NAME/KEY: MISC FEATURE
LOCATION: (45)...(45)
OTHER INFORWATION: Xaa at position 45 can be Leu or Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZZIF: 94080
COMPUTER READABLE FORM:
REDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M FC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION 124
PRIOR APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112, Application US/09056160B
; Sequence 112, Application US/09056160B
; Patent No. US2002002315Al
; GENERAL INFORMATION:
APPLICANT: Baca, Manuel
; APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA Way
CITY: SOUTH San Francisco
; CTY: SOUTH San Francisco
; COUVIRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                    APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazar, Gregory Alan
APPLICANT: Lazar, Gregory Alan
APPLICANT: Dasjarlais, John Rudolf
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REPERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT PILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR PILING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.2
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
       US20040110226A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 10; Conservative
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26 GYDFTHYGMN 35

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COMPUTE: USEN
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winhatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-89-2002
CLASSIFICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 06-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 44,637
REGISTRATION NUMBER: 44,637
REGISTRATION NUMBER: 44,637
REGISTRATION NUMBER: 44,637
TELECOMONICATION INFORMATION:
TELECOMONICATION:
TELECOMONICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: 110: US-10-234-671-110
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GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: April 25, 2006, 07:01:21; Search time 6.41509 Seconds (#without alignments)

Ferfect score: 62
Sequence: 1 GYDFTHYGMN 10

Scoring table: BLOSUM62

Scoring table: BLOSUM62

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Be: Published Applications AA New:*

1: /SIDS5/ptodata/1/pubpaa/US06 NEW PUB.pep:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW=PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/DCT_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/DCT_NEW_PUB.pep:*
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6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US00_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US00_NEW_PUB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIBS

					SOMMACIES	
Result No.	Score	Query Match	Length	DB	ΩI	Description
	62	100.0	118	9	US-10-648-816-10	Sequence 10, Appl
0	62	100.0	118	ø	US-10-648-816-12	
(M	62	100.0	118	ø	US-10-648-816-13	Sequence 13, Appl
4	62	100.0	121	9	US-10-648-816-16	-
·	62	100.0	123	7	US-11-208-422-12	Sequence 12, Appl
9	51	82.3	256	7	US-11-054-515-2080	•••
	51	82.3	256	7	US-11-266-444-2080	2080
60	48	77.4	92	7	US-11-240-195-84	84,
6	48	77.4	112	7	ч	20,
10	4.8	77.4	116	7	US-11-174-186-2	'n
11	48	77.4	116	7	US-11-174-186-4	4,
12	48	77.4	116	7	US-11-174-186-6	ģ
13	48	77.4	116	7	US-11-174-186-17	Sequence 17, Appl
14	48	77.4	116	7	US-11-174-186-18	Sequence 18, Appl
15	48	77.4	116	7	US-11-174-186-19	Sequence 19, Appl
16	48	77.4	116	7	US-11-174-186-20	Sequence 20, Appl
17	48	77.4	116	7	US-11-174-186-21	Sequence 21, Appl
18	48	77.4	116	7	US-11-174-186-22	
19	48	77.4	116	2	US-11-174-186-23	Sequence 23, Appl
20	48	77.4	116	7	US-11-174-186-24	_
21	48	77.4	116	7	US-11-174-186-25	Sequence 25, Appl
22	48	77.4	116	7	US-11-174-186-26	
23	48	77.4	117	7	US-11-174-186-35	35,
24	48	77.4	117	7	US-11-037-199-32	Sequence 32, Appl
25	48	77.4	118	9	US-10-648-816-9	Sequence 9, Appli

Sequence 14, Appl Sequence 15, Appl Sequence 7, Appli Sequence 31, Appl	a L L	Sequence 10, Appl Sequence 89, Appl Sequence 41, Appl Sequence 58, Appl	Sequence 58, Appl Sequence 31, Appl Sequence 33, Appl Sequence 68, Appl	70, 848, 848,
9944	US-11-240-195-52 US-11-240-195-111 US-11-240-195-109 US-11-208-422-8	US-11-208-422-10 US-11-240-195-89 US-11-174-186-41 US-11-084-558	US-11-004-330-33 US-11-136-250-58 US-10-512-184-31 US-10-512-184-33	10-512- 11-054- 11-266-
18 6 21 6 21 7 21 7	121 7 121 7 123 7 123 7	23 7 7 7 7 8 9 8 7	28633	329 6 248 7 248 7
		4446		
4444	4444	4444	4444	4 4 4 4 0 0 0 0
26 27 29	333333	3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	8 6 4 4 . 8 0 0 H 6	4444

ALIGNMENTS

RESULT 1 US-10-648-816-10 Sequence 10, Application US/10648816 Sequence 10, Application No. US20050244405A1 GENERAL INFORMATION: APPLICANT: Van Bruggen, Nicholas APPLICANT: Perrara, Napoleone TITLE OF INVENTION: and Uses Thereof TITLE OF INVENTION: and Uses Thereof FILE REPERENCE: P1717D1 CURRENT APPLICATION NUMBER: US/10/648,816 CURRENT APPLICATION NUMBER: US/09/718,694 PRIOR APPLICATION NUMBER: US/09/718,694 PRIOR FILING DATE: 2000-11-21 PRIOR FILING DATE: 1998-12-22 NUMBER OF SEQ ID NOS: 16 SEQ ID NO 10 LENGTH: 118 TYBE: PRT CREATE: PRT CRE	US-10-648-816-10 Query Match 100.0%; Score 62; DB 6; Length 118; Best Local Similarity 100.0%; Pred. No. 0.00093; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 GYDFTHYGMN 10 Db 26 GYDFTHYGMN 35	RESULT 2 US-10-648-816-12 US-10-648-816-12 ; Sequence 12, Application US/10648816 ; Publication No. US20050244405A1 ; GENERAL INFORMATION: ; APPLICANT: Van Brugen, Nicholas ; APPLICANT: Perrara, Napoleone ; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists ; TITLE OF INVENTION: and Uses Thereof ; TITLE OF INVENTION: and Uses Thereof ; CURRENT APPLICATION NUMBER: US/10/648,816 ; CURRENT FILING DATE: 2003-08-26 ; PRIOR APPLICATION NUMBER: US/99/718,694 ; PRIOR PILING DATE: 1998-11-21 ; PRIOR FILING DATE: 1998-12-22
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Gaps

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APPLICANT: Ademand Camellia W.
APPLICANT: Ademand Camellia W.
APPLICANT: Lien, Samantha
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Meng, Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION FILE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION FILE OF INVENTION: DOLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION FILE OF INVENTION: DOLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION FILE OF REPLICATION NUMBER: US 60/603,057
PRIOR FILING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 12
LENGTH: 123
LENGTH: 123
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
FEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-054-51b-2080
US-11-054-51b-2080
US-11-054-51b-2080
US-11-054-51b-2080
Publication No. US2005025532A1
GENERAL INPORMATION:
I TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523B3
CURRENT PELING DATE: 2005-02-10
FRIOR PELING DATE: 2006-02-11
FRIOR PILING DATE: 1004-06-18
FRIOR FILING DATE: 2004-06-18
FRIOR FILING DATE: 2004-06-18
FRIOR FILING DATE: 2001-11-4
FRIOR FILING DATE: 2001-11-4
FRIOR FILING DATE: 2001-11-16
FRIOR FILING DATE: 2001-12-19
FRIOR FILING DATE: 2001-12-19
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-03-16
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
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Indels
        ö
    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/11208422
Publication No. US20060067930A1
GENERAL INFORMATION:
    10; Conservative
                                                                                 1 GYDFTHYGMN 10
                                                                                                                                                      26 GYDPTHYGMN 35
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                                                                                                                                                                                                                                                                                 RESULT 5
US-11-208-422-12
        Matches
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Sequence 13, Application US/10648816

Publication No. US20050244405A1

GENERAL INFORMATION:

APPLICANT: Van Bruggen, Nicholas

APPLICANT: Ferrara, Napoleone

TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists

TITLE OF INVENTION: and Uses Thereof

FILE REFERENCE: P1717D1

CURRENT FILING DATE: 2003-08-26

PRIOR APPLICATION NUMBER: US/09/718,694

PRIOR APPLICATION NUMBER: US/09/718,694

PRIOR APPLICATION NUMBER: US/09/218,481

PRIOR APPLICATION NUMBER: US/09/218,481

PRIOR FILING DATE: 2000-11-21

PRIOR FILING DATE: 2000-11-21

PRIOR FILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 13

LENGTH: 118
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; Sequence 16, Application US/10648816
; Sequence 16, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INPORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Perrara, Napoleone
; TITLE OF INVENTION: Vand USes Thereof
; TITLE OF INVENTION: Vand USes Thereof
; TITLE OF INVENTION: VANBER: US/10/648,816
; CURRENT APPLICATION NUMBER: US/09/718,694
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR PILING DATE: 2000-11-21
; PRIOR PILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 62; DB 6; Length 118; Best Local Similarity 100.0%; Pred. No. 0.00093; Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 62; DB 6; Length 11
100.0%; Pred. No. 0.00093;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 10; Conservative
    NUMBER OF SEQ ID NOS: 16
SEQ ID NO 12
LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 GYDFTHYGMN 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-648-816-13
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ORGANISM: Homo sapiens
                                                                                                                                                               ORGANISM: Homo sapiens US-10-648-816-12
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Best Local Similarity
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                                                                                                                                  TYPE: PRT
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JEGQUEGNCE 20, Application US/11240195

Publication No. US20060057140A1

JERNERAL INFORMATION:

APPLICANT: FEMERATEDN:

ANTICOAGULANT AGENTS USEFUL IN TREATMENT

TITLE OF INVENTION: OF THROMBOSIS

FILE OF PARTICATION NUMBER: US/11/240,195

PRIOR FILING DATE: 2003-05-05

PRIOR FILING DATE: 1999-08-07

PRIOR PRILING DATE: 1997-01-06

PRIOR PRILING DATE: 1997-01-06

PRIOR PRILING DATE: 1997-01-06

PRIOR PRILING DATE: 1997-01-06

PRIOR PRILING DATE: 1997-01-07

PRIOR PRINGRAPHICATION NUMBER: 60/029,119

PRIOR PRINGRAPHICATION NUMBER: 60/029,119

PRIOR PRINGRAPHICATION NUMBER: 09/010,108

PRIOR PRINGRAPHICATION NUMBER: 09/010,109

PRIOR PRINGRAPHICATION NUMBER: 09/010,109

PRIOR PRINGRAPHICATION N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.4%; Score 48; DB 7; 80.0%; Pred. No. 0.18; tive 1; Mismatches
                               PRIOR FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 09/344,050
PRIOR PLING DATE: 1999-06-25
PRIOR PLING DATE: 1999-06-25
PRIOR PLING DATE: 1997-01-06
PRIOR PRILING DATE: 1997-01-06
PRIOR PILING DATE: 1996-01-17
PRIOR PILING DATE: 1996-01-17
PRIOR PILING DATE: 1996-10-24
NUMBER OF SEQ ID NOS: 111
SEQ ID NO 84
APPLICATION NUMBER: 10/051,852
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Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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3 GYTFTNYGMN 12
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ORGANISM: Homo sapiens
US-11-240-195-20
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CRGANISM: Homo sapiens
US-11-240-195-84
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is sequence 2080, Application US/11266444

is bedience 2080, Application No. US20060062789A1

is cannot no. US2006-11-04

is prior application no. US2006-11-04

is prior application no. US2006-11-17

is prior application no. US2006-10-17

is prior prior no. US2006-10-17

is prior prior no. US2006-10-17

is prior application no. US2006-10-17

is prior applicatio
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; Sequence 84, Application US/11240195
; Publication No. US20060057140A1
; GENERAL INFORMATION:
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
; FILE REFERENCE: PSOB16-1
; CURRENT APPLICATION NUMBER: US/11/240,195
; CURRENT APPLICATION NUMBER: US/10/430,176
; PRIOR PILING DATE: 2003-05-05
; PRIOR PLING DATE: 2001-03-27
; PRIOR PILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/359,202
; PRIOR PILING DATE: 1999-07-22
; PRIOR PILING DATE: 1999-07-22
; PRIOR FILING DATE: 1998-08-07
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                                                                                                                                                                                                                                      DB 7; Length 256;
                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                  Query Match 82.3%; Score 51; DB 7;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           1 GYDPTHYGMN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GYPFTHYGWN 35
                                                  ; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2080
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CRGANISM: Homo sapiens
US-11-266-444-2080
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                   SEQ ID NO 2080
LENGTH: 256
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LOCATION: (16)..(16)
OTHER INFORMATION: wherein Xaa at position 16 is a glutamic acid or a serine
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genemee 4, Application US/11174186

publication No. US20050244418A1

genemee 4, Application No. US20050244418A1

geneme 5, Rin-Ming

APPLICANT: Gillies, Stephen

TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

FILE REFERENCE: LEX-019

CURRENT APPLICATION NUMBER: US/11/174,186

CURRENT FILING DATE: 2005-07-01

PRIOR PELING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42

SEQ ID NO 4

LENGTH: 116
RESULT 10
US-11-174-186-2
i Sequence 2, Application US/11174186
j Publication No. US20050244418A1
j GENERAL INFORMATION:
i APPLICANT: Gallies, Stephen
j APPLICANT: Qian, Xiugi
j TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
j TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
j TITLE OF INVENTION Recombinant Tumor Specific Antibody And Use Thereof
j FILE REPERENCE: LEX-019
j CURRENT FILING DATE: 2005-07-01
pRIOR PELING DATE: 2005-07-01
j PRIOR PELING DATE: 2001-05-03
j NUMBER OF SEQ ID NOS: 42
j SOFTWARE: Patentin version 3.3
j SEQ ID NO 2
l LENGTH: 116
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LOCATION: (2)...(2)
OTHER INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (9)...(9).
OTHER INFORMATION: wherein Xaa at position 9 is a proline or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ION: (11)..(11)
INFORMATION: wherein Xaa at position 11 is a leucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: variable heavy chain sequence in the EpCAM antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 7; Length 116;
Pred. No. 0.23;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-174-186-2
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LOCATION: (73)...(73)
OTHER INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
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OTHER INFORMATION: wherein Xaa at position 69 is an alanine, a threonine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (80)..(80)
OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (46)..(46).
OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at position 68 is a phenylalanine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (84)...(84)
OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
                                                                                                                                                                                                                                                       LOCATION: (40)..(40)
OTHER INFORMATION: wherein Xaa at position 40 is a threonine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an alanine or a threonine
                                                                                                                        LOCATION: (38)...(38)
OTHER INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
LOCATION: (17)..(17)
OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (43)...(43)
OTHER INFORMATION: wherein Xaa at position 43 is a lysine or a glutamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (71)..(71)

THER INFORMATION: wherein Xaa at position 71 is a serine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (72)...(72)
OTHER INFORMATION: wherein Xaa at position 72 is a leucine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an alanine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (65)..(65)
OTHER INFORMATION: wherein Xaa at position 65 is a lysine or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (76)..(76)
OTHER INFORMATION: wherein Xaa at position 76 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at position 79 is
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OTHER INFORMATION: wherein Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (68)..(68)
OTHER INFORMATION: wherein Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KBY: misc feature
                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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LOCATION: (68)..(68)
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LOCATION: (85)..(85)
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FEATURE:
NAME/KEY: misc_feature
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NAME/KEY: misc feature
LOCATION: (100)..(100)
OTHER INFORMATION: wherein Xaa at position 100 is an isoleucine or a methionine
                             PRATURE:
NAME/KRX: misc_feature
NAME/KRX: misc_feature
LOCATION: (88). (88)
OTHER INPORMATION: wherein Xaa at position 88 is an asparagine, an alanine or
OTHER INFORMATION: serine
                                                                                                                                               FEATURE:
NAME/KBY: misc_feature
LOCATION: (91)...(91)
OTHER INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (108).
OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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| Sequence 6, Application US/11174186
| Publication No. US20050244418A1
| GENERAL INFORMATION:
| APPLICANT: 10, Kin-Ming
| APPLICANT: 10, Kin-Ming
| APPLICANT: 10, Kin-Ming
| TITLE OF INVERTION: Recombinant Tumor Specific Antibody And Use Thereof
| TILE REFERENCE: LEX-019
| TILE REFERENCE: LEX-019
| CURRENT APPLICATION NUMBER: US/11/174,186
| CURRENT PILING DATE: 2005-07-01
| PRIOR PILING DATE: 2001-05-03
| NUMBER OF SEQ ID NOS: 42
| SOFTWARE: Patentin version 3.3
OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEATURE:
NAME/KEY: misc feature
LOCATION: (111)..(111)
OTHER INFORMATION: wherein Xaa at position 111 is a serine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ON: (2)..(2)
INFORMATION: wherein Xaa at position 2 is an isoleucine or a valine
                                                                                                                                                                                                                                                                                          at position 9 is a proline or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (11)...(11)
OTHER INFORMATION: wherein Xaa at position 11 is a leucine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
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Pred. No. 0.23;
1; Mismatches 1; Indels
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LOCATION: (9)._(9)
OTHER INFORMATION: wherein Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYDFTHYGMN 10
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LOCATION: (73)...(73)
OTHER INFORMATION: wherein Xaa at position 73 is a glutamic acid or an aspartic acid
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OTHER INFORMATION: wherein Xaa at position 70 is a phenylalanine or an isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (88):..(88):..
OTHER INFORMATION: wherein Xaa at position 88 is an asparagine, an alanine or a
OTHER INFORMATION: serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (80)..(80)
OTHER INFORMATION: wherein Xaa at position 80 is a phenylalanine or a tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (63)..(63)
OTHER INFORMATION: wherein Xaa at position 63 is an aspartic acid or a lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ION: (91)..(91) INFORMATION: wherein Xaa at position 91 is a methionine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (68)...(68)
OTHER INFORMATION: wherein Xaa at position 68 is a phenylalanine or a valine
                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (46)...(46)
OTHER INFORMATION: wherein Xaa at position 46 is a lysine or a glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ION: (83)...(83)
INFORMATION: wherein Xaa at position 83 is an isoleucine or a leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (69)...(69)
OTHER INFORMATION: wherein Xaa at position 69 is an alanine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (76)..(76)
OTHER INFORMATION: wherein Xaa at position 76 is an alanine or a threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (84)...(84)
OTHER INFORMATION: wherein Xaa at position 84 is an asparagine or a serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (85)...(85)
OTHER INFORMATION: wherein Xaa at position 85 is an asparagine or a serine
                                                                                                                                                                                                                                                                       at position 40 is a threonine or an alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (93)...(93)
OTHER INFORMATION: wherein Xaa at position 93 is a threonine or a valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (17)..(17)
OTHER INFORMATION: wherein Xaa at position 17 is a threonine or a serine
                                                                                                                             LOCATION: (38)...(38)
OTHER INFORMATION: wherein Xaa at position 38 is a lysine or an arginine
                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (40) ... (40)
OTHER INFORMATION: wherein Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
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1 GYDFTHYGMN 10
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; LOCATION: (108)...(108); OTHER INFORMATION: wherein Xaa at position 108 is a glutamine or a threonine US-11-174-186-6
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US-11-74-186-17
i Sequence 17, Application US/11174186
j Publication No. US20050244418A1
i GENERAL INFORMATION:
APPLICANT: G111les, Stephen
j APPLICANT: Q1an, Xiugi
j TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
TITLE OF INVENTION: NUMBER: US/11/174,186
j FILE REPERENCE: LEX.019
j CURRENT APPLICATION NUMBER: US 60/288,564
j PRIOR PILLING DATE: 2005-07-01
j PRIOR PILLING DATE: 2001-05-03
j NUMBER OF SEQ ID NOS: 42
j SEQ ID NOS: 42
j SEQ ID NO 17
LENGTH: 116
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| Publication No. US20050244418A1 |
| GENERAL INPORMATION: |
| APPLICANT: Gillies, Stephen |
| APPLICANT: Lo, Kin-Ming |
| APPLICANT: Lo, Kin-Ming |
| APPLICANT: Lo, Kin-Ming |
| TILLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof |
| FILE REFERENCE: LEX-019 |
| FILE REPERENCE: LE
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                                                                                                                                                        Query Match

77.4%; Score 48; DB 7; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.23;
Matches 8; Conservative 1; Mismatches 1; Indels
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Pred. No. 0.23;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: VH6 heavy chain US-11-174-186-17
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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26 GYTFINYGMN 35
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ORGANISM: Artificial
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ORGANISM: Artificial
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US-11-174-186-18
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Gaps

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NSOLI-174-186-19
(NS-11-174-186-19
) Sequence 19, Application US/11174186
) Sequence 19, Application US/11174186
) Sequence 19, Application US/11174186
) GENERAL INFORMATION:
) APPLICANT: Gillies, Stephen
) APPLICANT: Qian, Xiugh
) APPLICANT: Qian, Xiugh
) TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
) TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
) TITLE OF INVENTION: Becombinant Tumor Specific Antibody And Use THEREOF TITLE OF TOWNERS: US/11/174,186
) CURRENT PILLING DATE: 2005-07-01
) PRIOR PILLING DATE: 2001-05-03
) NUMBER OF SEQ ID NOS: 42
) SOFTWARE: PATENTIN Version 3.3
) SEQ ID NOS: 42
) SOFTWARE: PATENTIN Version 3.3
) SEQ ID NOS: 42
) SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 80.0 Matches 8; Conservative
26 GYTFTNYGMN 35
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US-10-764-428-19 64 1 GYSITSGYSWN 11 Title: Perfect score: Sequence:

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2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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geneseqp1980s:* A_Geneseq 21:* Database

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SUMMARIES

	Description	Adg90715 Anti-VEGF	Aaw95656 Mus muscu	Aaw95657 Mus muscu	Aab76946 Variable		m	-	Adw00654 Human ant	Adw00655 Human ant	Adw79890 Anti-IgE	Adw79889 Anti-IgE	Aao20095 Protein e	Aaw95647 Mus muscu	Aaw95648 Mus muscu	Aab76936 Variable	Aab76937 Variable	Adn07024 Murine an	Adn07023 Murine an	Adw00645 Murine Ma		Aar33306 MaB11 hea	Aay85194 Heavy cha	Aaw95666 Mus muscu	Aaw95665 Mus muscu
	a	ADQ90715	AAW95656	AAW95657	AAB76946	AAB76945	ADN07033	ADN07032	ADW00654	ADW00655	ADW79890	ADW79889	AA020095	AAW95647	AAW95648	AAB76936	AAB76937	ADN07024	ADN07023	ADW00645	ADW00646	AAR33306	AAY85194	AAW95666	AAW95665
	DB	8	~	~	4	4	80	8	σ	0	6	6	m	7	~	4	4	8	æ	σ	σ	~	m	7	7
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*	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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>>41			Adw79899 Anti-1gE Adw79898 Anti-1gE Aaw95671 Mus muscu Aaw95670 Mis miscu	Vari	Adno7047 Anti-IgB Adw00669 Human ant Adw00669 Human ant Adw79903 Anti-IgB
AAB76954 AAB76955 ADN07041	ADN07067 ADN07042 ADW00664 ADW00663	ADW00689 ADW00694 ADW00693	ADW79899 ADW79898 AAW95671	AAB76959 AAB76960 AAB76960 ADN07046	3 ADN07047 3 ADW00668 3 ADW00669 4 ADW79903
229 4 229 4 229 8	2229 2229 2229 2239	2229	2222	22222	22333 23333 23333
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25 26 27	228 3398 1098	. m m m . m m 4	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	2 6 4 4 2 0 0 H	4 4 4 4 6 6 4 7

ALIGNMENTS

Anti-VEGF antibody heavy chain HVR1 peptide SEQ ID NO:19. ADQ90715 standard; peptide; 11 AA. 21-OCT-2004 (first entry) ADQ90715;

antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antiinflammatory; antianglogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; anti-VEGF antibody; anti vascular endothelial cell growth factor antibody; heavy chain; HVR1.

Homo sapiens. Synthetic.

WO2004065417-A2.

05-AUG-2004.

23-JAN-2004; 2004WO-US001844.

23-JAN-2003; 2003US-0442484P.

(GETH) GENENTECH INC.

Simmons L;

WPI; 2004-562149/54.

Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.

Claim 13; SEQ ID NO 19; 161pp; English.

The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid

us-10-764-428-19.rag

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cc the amino acid found at the corresponding PR position of a human subgroup variable domain consensus sequence that has a hypervatable region 1 (HVR1) and/or HVR2 amino acid sequence that has a hypervatable region 1 (HVR1) and/or HVR2 amino acid sequence with the most sequence identity with a corresponding HVR1 and/or HVR2 sequence of the variable domain.

CC The antibody or antigen binding fragment variable domain comprises the modified antibody or antigen-binding fragment. The antibody and antigen binding fragment to antibody and antigen binding fragment are useful for cumodified antibodies or antigen-binding fragment. The antibody and antigen binding fragment invention are useful for methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in conditing fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and composition and immunological disorders. The present sequence represents a heavy chain HVR1 peptide of an anti-VEGF (vascular cendothelial cell growth factor) antibody, which is used in the central invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variable heavy chain; IgB; antibody; anti-IgB; reduction; prevention; histemine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic thintis; conjunctivitis; hay fever; eccema; anaphylactic shock; urticaria.
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100.0%; Pred. No. 0.00063;
ive 0; Mismatches 0;
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The sequence is that of the variable heavy chain of e27. It was used as part of a method to improve the affinity of anti-IgB antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgB mediated production of histamine in a mammal. They can be

Disclosure; Page 90-91; 129pp; English.

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used for treating a disorder mediated by IgB such as hypersensitivity, atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Improving affinity of polypeptides, particularly anti-IgB antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                                                                                                                                                                                                                                                                               Variable heavy chain; IgB; antibody; anti-IgB; reduction; prevention; histemine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
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                                                                                                                                                                                                                                                                                                                                                                   Mus musculus anti-IgB e25, e26 & e426 variable heavy chain.
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                                                                                                                                                                                                                                                                             AAW95657 standard; protein; 114 AA.
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les 11; Conserv
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Antibody, antiasthmatic, antiallergic, ophthalmological, dermatological, antinflammatory; Ig E, immunoglobulin E, asthma; allergic rhinitis, conjunctivitis, eczema, urticaria, food allergy.

Variable heavy chain sequence of e27 SEQ ID 11.

(first entry)

17-APR-2001

AAB76945;

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This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgB antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-IgB (immunoglobulin B) antibody; b) substituting alternative residues to create candidate molecules, and c) substituting alternative residues to create candidate molecules, and c) caspacing those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic, ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgB-mediated disorders such as sathma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned concletc acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Anno acid sequences AAB76936.

AAB76960 represent fragments of anti-IgB antibodies of the invention. Polymucleotide sequence AAF69253 represents an expression plasmid used in the generation of affinity improved anti-IgB antibodies
                                                                                                                                                                                                                                                                                                                                                                                                 Antibody, antiasthmatic, antiallergic, ophthalmological, dermatological, antinflammatory, Ig B, immunoglobulin B, asthma; allergic rhinitis, conjunctivitis, eczema; urticaria, food allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding anti-immunoglobulin B antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity
                                                                                                                                                                                                                                                                                                                            Variable heavy chain sequence of e25, e26 and e426 SEQ ID 12.
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                                                                         AAB76946 standard; protein; 114 AA.
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RESULT 4
                                               AAB76946
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New nucleic acid encoding anti-immunoglobulin B antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin B prone to isomerization by other residues by affinity maturation with phage display.

Disclosure; Fig 2; 87pp; English.

Lowe J;

Jardieu PM,

Presta LG,

Lowman HB,

WPI; 2001-122353/13.

(GETH) GENENTECH INC

02-JUL-1997; 30-JUN-1998;

98US-00109207. 97US-0051554P.

US6172213-B1 09-JAN-2001.

Synthetic.

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This invention relates to a nuclectide sequence encoding an antibody with improved anti-IgE antibody activity. The antibody has improved action due comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallargic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IGE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide sequence AAF69253 represents an expression plasmid used in the course of the invention, and oligonucleotides AAF69254 - AAF69271 are used in the generation of affinity improved anti-1gB antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN07033 standard, protein; 114 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 114 AA;
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11; Conservative 1 GYSITSGYSWN 11

Best Local Similarity Matches 11, Conserv

GYSITSGYSWN

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AAB76945 standard; protein; 114 AA.

RESULT 5

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Key Region Region Region

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Chemotherapy, IgB-mediated disorder; asthma; allergic rhinitis; eczema; urticaria; food allergy; hypersensitivity; anaphylactic hypersensitivity; antiasthmatic; antiallergic; dermatological; antibacterial; immune disorder; inflammation; ear disease; nose disease; throat disease; respiratory disease; antiinflammatory; dermatological disease; immunosuppressive; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                        New composition of an improved anti-IgE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable heavy chain domain (VH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "CDR (Complementarity-determining region)-ni"
99. .110
/note= "CDR (Complementarity-determining region)-H3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .66
:e= "CDR (Complementarity-determining region)-H2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "CDR (Complementarity-determining region)-H1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human anti-IgB antibody e27 heavy chain variable region protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 64; DB 8;
100.0%; Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                                                      Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 11; 89pp; English.
                                                                                                                                                                                                                                                                                                                                      Jardien PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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26. .36
/label= CDR-H1
51. .66
/label= CDR-H2
                                                                                           /label= CDR-H3
                                                                                                                                                                                                                                           97US-0051554P.
                                                                                                                                                                                                        17-NOV-2000; 2000US-00716028
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                                                                       .110
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                                                                                                                                                                                                                                                                                                                                      Presta LG,
                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-326922/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                           02-JUL-1997;
30-JUN-1998;
                                                                                                                                US6723833-B1
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                                                                                                                                                                     20-APR-2004
                                                                                                                                                                                                                                                                                                                                      Lowman HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADW00654;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition of an improved anti-IgE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable heavy chain domain (VH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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 Anti-IgB antibody, immunosuppressive agent, IgB-mediated disorder; therapy, atopic allergy; anaphylactic hypersensitivity; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy; variable heavy chain domain; VH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 64; DB 8; Length 114;
100.0%; Pred. No. 0.0083;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-IgE antibody e27 variable heavy chain domain (VH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 12; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jardieu PM,
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN07032 standard; protein; 114 AA.
                                                                                                                                                     26. .36
/label= CDR-H1
51. .66
/label= CDR-H2
                                                                                                                                                                                                                                               /label= CDR-H3
                                                                                                                                                                                                                                                                                                                                                                                               97US-0051554P.
98US-00109207.
                                                                                                                                                                                                                                                                                                                                                            2000US-00716028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-326922/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-1998;
                                                                                               Unidentified
                                                                                                                                                                                                                                                                                    US6723833-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-2004
                                                                                                                                                                                                                                                                                                                         20-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lowman HB,
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Best Loca Matches

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Location/Qualifiers

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Gaps

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Length 114; 0; Indels Lowe

23-DEC-2004

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Antiasthmatic; Respiratory-Gen.; CNS-Gen.; Hypotensive; Antiinflammatory; Antimicrobial; Antiallergic; Cardiant; Analgesic; Vasotropic; asthma; chronic obstructive pulmonary disease; respiratory disease; pulmonary disease; cystic fibrosis; dyspnea; emphysema; pulmonary hypertension; pulmonary fibrosis; hyperresponsiveness of the airways; infectious diseases; respiratory tract inflammation; chronic bronchitis; respiratory distress syndrome; pain; allergic rhinitis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-1g8 antibody e26/e426/e25 heavy chain CDR domain fragment, SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for treating an IgB-mediated disorder. The method involves administering a therapeutical amount of an anti-IgB antibody or its IgB binding fragment. The invention is useful for treating an IgB-mediated disorder e.g. asthma, allergic rhinlis, eczema, utticaria, food allergies and hypersensitivity e.g. anaphylactic hypersensitivity. The present sequence is the human anti-IgB antibody e26, e27 and e426 variable heavy chain protein.
                                                                                                                                                                                                                                            Treating an IgB-mediated disorder, e.g. asthma, allergic rhinitis, eczema, urticaria, food allergies, or hypersensitivity, by administering an anti-IgB antibody or its antigen-binding fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 64; DB 9; Length 114; 100.0%; Pred. No. 0.0083; Pred. 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin E; IgE; antibody; antibody therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 12; 92pp; English.
                                                                                                                                                                    Jardieu PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADW79890 standard; protein; 114 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JUL-2003; 2003US-0492231P.
                                       02-JUL-1997; 97US-0051554P.
30-JUN-1998; 98US-00109207.
17-NOV-2000; 2000US-00716028.
02-MAR-2004; 2004US-00791619.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
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                                                                                                                                                                      Presta LG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ROBI/) ROBINSON C B. (BALL/) BALL H A.
                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYSITSGYSWN
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                                                                                                                                                                                                              WPI; 2005-038757/04.
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Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2005
                                                                                                                                                                      Lowman HB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemotherapy, IgB-mediated disorder; asthma; allergic rhinitis; eczema; urticaria; food allergy; hypersensitivity; anaphylactic hypersensitivity; antiasthmatic; antiallergic; dermatological; antibacterial; minemune disorder; inflammation; ear disease; nose disease; throat disease; respiratory disease; antiinflammatory; dermatological disease; immunosuppressive; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for treating an IgB-mediated disorder. The method involves administering a therapeutical amount of an anti-IgB antibody or its IgB binding fragment. The invention is useful for treating an IgB-mediated disorder e.g. asthma, allergic rhinitis, eczema, urticaria, food allergies and hypersensitivity e.g. anaphylactic hypersensitivity. The present sequence is the human anti-IgB antibody e27 heavy chain variable region protein.
                                                                                                                                                                                                                                                                                                                                                              Treating an IgB-mediated disorder, e.g. asthma, allergic rhinitis, eczema, urticaria, food allergies, or hypersensitivity, by administering an anti-IgB antibody or its antigen-binding fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human anti-IgB antibody e26, e27 and e426 variable heavy chain protein.
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hote= "CDR (Complementarity-determining region)-Hl"
51. .66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 64; DB 9; Length 114;
100.0%; Pred. No. 0.0083;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                    Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 11; 92pp; English
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                                                                                                                                                                                                                                                                                    Jardien PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADW00655 standard; protein; 114 AA.
                                                                                                                                                     02-JUL-1997; 97US-0051554P.
30-JUN-1998; 98US-00109207.
17-NOV-2000; 2000US-00716028.
                                                                                                               2004US-00791619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100 nes 11; Conservative
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                                                                                                                                                                                                                                                                                    Lowman HB, Presta LG,
                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                           WPI; 2005-038757/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 114 AA;
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                                US2004259077-A1
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                                                                                                                 02-MAR-2004;
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Query Match

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ADW00655;

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Region Region Region

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The present invention relates to compositions comprising a carrier, a first active agent comprising non-glucocorticoid steroids or their salts and a second active agent comprising an anti-immunoglobulin B (IgE) antibody effective to treat asthma, chronic obstructive pulmonary disease.

The compositions are also useful for reacting pulmonary disease. The compositions are useful for respiratory, lung/malignant disorder/condition such as asthma, chronic obstructive pulmonary disease, cystic fibrosis, dyspme, emphysema, chronic obstructive pulmonary hypertension, quilmonary pulmonary diseases, cystic fibrosis, dyspme, emphysema, chronic obstructive pulmonary diseases, cystic fibrosis, dyspme, emphysema, chronic constructive pulmonary hypertension, quilmonary binonchoconstriction, crespiratory tract inflammation or allergis, bronchoconstriction, difficult chapting, impeded or obstructed lung airways, adenosine test for cardiac function, pulmonary vasoconstriction, impeded respiratory distress syndrome, administration of adenosine creating, cancer or chronic bronchitis, and for reducing levels largic rhinitis, cancer or chronic bronchitis, and for reducing levels incaring an allergic rhinitis, cancer or chronic bronchitis, and for reducing levels incaring an allergic rhinitis, cancer or chronic bronchitis, and for reducing levels incaring an allergic rhinitis or adenosine or adenosine cest for cardiac incared anti-IgE antibody CDR domain, used to illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antiasthmatic; Respiratory-Gen.; CNS-Gen.; Hypotensive; Antiinflammatory; Antimicrobial; Antiallergic; Cardiant; Analgesic; Vasotropic; asthma; chronic obstructive pulmonary disease; respiratory disease; pulmonary disease; respiratory disease; pulmonary disease; cystic fibrosis; dyspnea; emphysema; pulmonary hypertension; pulmonary fibrosis; hyperresponsiveness of the airways; infectious diseases; respiratory tract inflammation; chronic bronchitis; respiratory distress syndrome; pain; allergic rhinitis; cancer; immunoglobulin E; IgE; antibody; antibody therapy.
             Composition used for treating e.g. asthma, chronic obstructive pulmonary disease, cystic fibrosis, dyspnea, emphysema, pain, allergic rhinitis and cancer, comprises carrier, non-glucocorticoid steroids and anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-IgE antibody e27 heavy chain CDR domain fragment, SEQ ID 4.
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100.0%; Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                              Disclosure; SEQ ID NO 5; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADW79889 standard; protein; 114 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                  immunoglobulin E antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GYSITSGYSWN 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2005026881-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADW79889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The present invention relates to compositions comprising a carrier, a first active agent comprising non-glucocorticoid steroids or their salts and a second active agent comprising an anti-immunoglobulin B (IgE) antibody effective to treat asthma, chronic obstructive pulmonary disease.

Treducing the probability of or treating asthma and chronic obstructive pulmonary disease. The compositions are useful for centuring the probability of or treating asthma and chronic obstructive pulmonary disease, respiratory, lung/malignant disorder/condition such as asthma, chronic obstructive pulmonary disease, cystic fibrosis, dyspnea, emphysema, wheezing, pulmonary disease, cystic fibrosis, dyspnea, emphysema, chronic obstructive pulmonary diseases, cystic fibrosis, dyspnea, emphysema, chronic constructive pulmonary diseases, cystic fibrosis, dyspnea, emphysema, chronic construction, respiratory tract inflammation or allergies, lung surfactant or cappiratory tract inflammation or allergies, lung surfactant or usiquinone depletion, chronic bronchitis, bronchoconstriction, difficult cupiratory distress syndrome, administration, acute creptiratory distress syndrome, administration, acute creptiratory distress syndrome, administration of adenosine or adenosine creptiratory distress syndrome, administration of levels syndrome, pain, and for reducing levels of sensitivity to adenosine or adenosine or adenosine of sensitivity to adenosine or adenosine creptors. The present sequence of sensitivity to adenosine or adenosine used to illustrate the
                                                                                                             Composition used for treating e.g. asthma, chronic obstructive pulmonary disease, cystic fibrosis, dyspnea, emphysema, pain, allergic rhinitis and cancer, comprises carrier, non-glucocorticoid steroids and antimmunoglobulin E antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse monoclonal antibody; murine; surface antigen preSl epitope;
hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 64; DB 9; Length 114; 100.0%; Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by a 357nt DNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO20095 standard; protein; 119 AA.
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nes 11; Conservative
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                                     Robinson CB, Ball HA;
                                                                             WPI; 2005-161309/17.
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(BALL/) BALL H A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 114 AA;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Improving affinity of polypeptides, particularly anti-IgB antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                     antibody
                                                                                                                                   The invention relates to a changeable region of mouse monoclonal antibod recognising surface antigen preSI epitope of hepatitis B virus and gene. This sequence relates to a protein encoded by a 357nt DNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variable heavy chain; IgB; antibody; anti-IgB; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
                                                                                                                                                                                                                                                                                                   Gaps
                                            Changeable region of mouse monoclonal antibody recognizing surface antigen preS1 epitope of hepatitis B virus and gene.
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                                                                                                                                                                                                                                                                Length 119;
                                                                                                                                                                                                                                               100.0%; Score 64; DB 3; Length 11
100.0%; Pred. No. 0.0087; Lanat.cheB 0; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus anti-IgB MaB11 variable heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 85-86; 129pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW95647 standard; protein; 121 AA.
                                                                                                      Disclosure, Page 12, 14pp; Korean
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                                                                                                                                                                                                                                                                                                       11; Conservative
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2000-168375/15.
                                                                                                                                                                                                                                                                                  Local Similarity
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                N-PSDB; AAK99184
                                                                                                                                                                                                                                Sequence 119 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Improving affinity of polypeptides, particularly anti-IgB antibodies - by identifying appartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variable heavy chain; IgB; antibody; anti-IgB; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.
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                 Length 121;
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                                                               0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus anti-1gB F(ab)-2 variable heavy chain.
                     Score 64; DB 2;
Pred. No. 0.0088;
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                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 86, 129pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jardieu PM,
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                                                                                                                                                                                                                                                                                AAW95648 standard; protein; 121 AA.
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                     100.0%;
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Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
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This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgB antibody activity. The antibody has improved action due to a process comprising, a) identifying separtyl residues prone to isomerisation in unimproved anti-IgB (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiathmatic; antiallergic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgB-mediate disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned nucleic acids may also be used as affinity purification agents and in diagnostic assays for detecting the expression of an antigen of interest in specific cell, tissues or serum. Amino acid sequences AAB76936.

AAB7660 represent fragments of anti-IgB antibodies of the invention.

Polynucleotide sequence AAR69251 represents an expression plasmid used in the generation of affinity improved anti-IgB antibodies
                                                                                            Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological; antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding anti-immunoglobulin E antibody with improved properties, produced by substituting aspartyl residues in unimproved immunoglobulin E prone to isomerization by other residues by affinity
                                                       Variable heavy chain sequence of MaEll SEQ ID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Jardieu PM, Lowe J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 1; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                maturation with phage display
                                                                                                                                                                                                                                                                                                            98US-00109207.
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                 17-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lowman HB, Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI, 2001-122353/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                   02-JUL-1997;
                                                                                                                                                                                    Mus musculus.
                                                                                                                                                                                                                                                                                                            30-JUN-1998;
                                                                                                                                                                                                                           US6172213-B1
                                                                                                                                                                                                                                                                    09-JAN-2001.
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Query Match 100.0%; Score 64; DB 4; Length 121; Best Local Similarity 100.0%; Pred. No. 0.0088; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

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1 GYSITSGYSWN 11

8 8

26 GYSITSGYSWN 36

Search completed: April 25, 2006, 06:15:02 Job time : 60.7358 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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sw model OM protein - protein search, using April 25, 2006, 06:15:41; Search time 9.33962 Seconds (without alignments) 113.322 Million cell updates/sec Run on:

US-10-764-428-19 64 1 GYSITSGYSWN 11 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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DB	-	~		~													N					N	N	~	~	~	~	7	7
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A Query Match	92.2	0	0	90.6	90.6	87.5	87.5	84.4	84.4	4	4	~	N	H	•	78.1	9.9/	75.0	75.0	75.0	75.0	75.0	75.0	73.4	71.9	•	68.8	٠	٠
Score	59	28	28	28	28	26	99	54	54	54	54	23	53	52	25	20	49	48	48	48	48	4.8	48	47	46	45	44	43	43
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ALIGNMENTS

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RESULT	HVMS1B	Iq heavy

ig neavy cnain precurent v region (1204) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004 C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004 C;Accession: JT6508 R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J. J. Exp. Med. 169, 2007-2019, 1989 A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary A;Reference number: JT0501; MUID: 89279149; PMID: 2499554 A;Accession: JT0508 A;Reference muber: JT0501; MUID: 89279149; PMID: 2499554 A;Accession: JT0508 A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-116 < LEVY A;Coss-references: UNIPROT: P18532; UNIPARC: UPI00000278E1 A;Residues: J-116 < LEVY A;Residu

Gaps ö

Query Match 92.2%; Score 59; DB 1; Length 116; Best Local Similarity 90.9%; Pred. No. 0.007; Matches 10; Conservative 1; Mismatches 0; Indels

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1 GYSITSGYSWN 11 44 GYSITSGYSWH 54 ઠ 셤

RESULT 2 S26467

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Sacaro

90.6%; Score 58; DB 2; Length 104; 90.9%; Pred. No. 0.0092; Query Match Best Local Similarity

Begment

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A; Molecule type: DNA
A; Residues: 1-15, GY, 16-137 <R12>
A; Cross-references: UNIPARC:UPI000016CELC; EMBL:X07880; NID:951760; PIDN:CAA30727.1; PIDI
R;Jilka, R.L.; Pestka, G.
R;Jilka, R.L.; Pestka, G.
R;Jilka, R.L.; Pestka, G.
B;Jilka, M.I.; Acid. Sci. U.S.A. 74, 5692-5696, 1977
A;Title: Amino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin he
A;Reference number: A93814; MUID:78094475; PMID:414225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the heavy (alpha) chain of a mous
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A;Residues: 19-52, K',53-75, BYGB', 80-101, D', 103-106, ZB', 109-122, 124-137 <FRA>
A;Residues: 19-52, K',53-75, UNIPARC: UD10000173740
A;Cross-references: UNIPARC: UD10000173740
R;Hood, L.; Margolles, M.; Gavol, D.; Zakut, R.
unpublished results, cited by Padlan, B.A., Davies, D.R., Pecht, I., Givol, D., and Wrig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Contents: annotation; revision to residue 53
R;Cheadle, C.; Hook, L.E.; Givol, D.; Ricca, G.A.
Mol. Immunol. 29, 21-30, 1992
A;Title: Cloning and expression of the variable regions of mouse myeloma protein MOPC315.
A;Reference number: S23599; MUID:92114886; PMID:1731188
A;Accession: S23599
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*Residues: 19-137 «CHB»
A;Cross-references: UNIPARC:UDI0000113794; EMBL:X63972; NID:G53532; PIDN:CAA45384.1; PID
C;Comment: This alpha chain was isolated from a myeloma protein that has anti-dinitrophe
                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-137 <RIN>
A;Cross-references: UNIPROT:P01822; UNIPARC:UPI000002727B; GB:M27638; NID:g602706; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            figuration; 17. immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status experimental <81G>
F;19-136/Product: Ig heavy chain V region (WOPC 315) #status experimental <WAT>
F;33-116/Domain: immunoglobulin homology <1MM>
A; Title: Cloning, sequencing and expression of the rearranged MOPC 315 VH gene A; Reference number: PL0102; MUID:89238351; PMID:2497341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A,Residues: 1-14, 'H', 16-31 <JIL>
A,Residues: 1-14, 'H', 16-31 <JIL>
A,Cross-references: UNIPARC:UPI000017373E
A,Note: the authors translated mRNA in vitro to obtain the precursor protein
R;Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.
Fed. Proc. 38, 1839-1845, 1979
A;Title: Structure and function of immunoglobulin genes and precursors.
A;Reference number: A91462; MUID:79148758; PMID:428562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1, X', 3-11, X', 14-21 <SCH>
A;Cross-references: UNIPARC:UP1000017313F
A;Note: the authors translated mRNA in vitro to obtain the precursor protein
R;Francis, S.H.; Leslie, R.G.Q.; Hood, L.; Eisen, H.N.
Proc. Natl. Acad. Sci. U.S.A. 71, 1123-1127, 1974
A;Title: Amino-acid sequence of the variable region of the heavy (alpha) chai
A;Reference number: A93787; MUID:74170779; PMID:4524622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 137;
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Pred. No. 0.012;
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                                                                                                                                                                                                                                             A;Experimental source: strain MOPC 315
R;Rinfret, A; Dorrington, K.J.; Klein, M.
Rmitted to the EMBL Data Library, June 1988
A;Reference number: S03262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
A25114
Ig heavy chain V region (HP22, HP27) - mouse
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Matches 10; Conserv
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Cispecies: Mus musculus (house mouse)
Cispecies: Musculus (house)
Cispe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           during the primary
                                                                                                                                                                                                                                                                                                                                                     Inversor that precursor V region (M315) - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C; Accession: JT0509
R; Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A; Title: Early onset of somatic mutation in immunoglobulin VH genes during the p A; Reference number: JT0501; MUID:89279149; PMID:2499654
A; Accession: JT0509
A; Reference number: JT0501; MUID:89279149; PMID:2499654
A; Accession: JT0509
A; Residues: 1-116 < LEV
A; Residues: 1-116 < LEV
A; Csperiental source: strain BALB/C)
C; Superfamily: immunoglobulin
C; Superfamily: immunoglobulin
C; Superfamily: immunoglobulin
F; 1-18/Domain: signal sequence #status predicted <NAT>
F; 19-116/Product: Ig heavy chain V region (M315) #status predicted <NAT>
F; 33-116/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C;Accession: PLO102; S03262; A93814; A91462; A93787; S23599
R;Rinfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.
            Gaps
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Pred. No. 0.011;
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Pred. No. 0.01;
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Best Local Similarity 90.9
Matches 10, Conservative
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Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C;Accession: T01262
R;Pirofski, L.A.; Thomas, B.K.; Scharff, M.D.
A;DS Res. Hum. Retroviruses 9, 41-49, 1993
A;Title: Variable region gene utilization and mutation in a group of neutralizing murin-A;Reference number: Z14285; MUD:93152285; PMID:7678971
A;Accession: T01262
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A;Molecule type: mRNA
A;Residues: 1-114 <PIR.
A;Residues: 1-114 <PIR.
Cross-references: UNIPARC:UPIO000117638; EMBL:S54194; NID:g264864; PIDN:AAB25246.2; P:Cssuperfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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CjSpecies: Mus musculus (house mouse)

CjDate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

CjAccession: S38718

RjCimanis, A.Y.

submitted to the EMBL Data Library, November 1993

A;Reference number: S38713

A;Accession: S38718

A;Accession: S38718

A;Accession: Syeliminary

A;Molecule type: mRNA
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26464
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Accession: S26464
A;Accession: S26464
A;Accession: S26464
A;Accession: Library
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Pred. No. 0.047;
1; Mismatches
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Pred. No. 0.044;
1; Mismatches
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81.8%;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity 81.0
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             9; Conservative
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T01262
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[5] Species: Mus musculus (house mouse)

[6] Species: Mus musculus (house mouse)

[7] Cjate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999

[7] Accession: 830752

[8] Richart, P.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.

[8] Mucleic Acids Res. 15, 5496, 1987

[8] Aritle: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.

[8] Aritle: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.

[8] Aritle: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.

[8] Aritle: Improved RNA sequencing method to determine immunoglobulin homology

[8] Aritle: Immunoglobulin homology arithmose immunogl
                     C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000
C;Date: 29-Aug-1987 #sequence_revision 6.; Theze, J.; Fougereau, M.
ENBO J. 4, 3681-3688, 1985
A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin A;Reference number: A91028; MUD:86136012; PMID:3937730
A;Accession: A25114
A;Accession: A25114
A;Residues: 1-120 < OLL>
A;Coss-references: UNIPARC:UPI0000115D15; GB:X03374; NID:951983; PIDN:CAA27071.1; PID:95;Superfamily: immunoglobulin | munnoglobulin homology | munnoglobulin | F;15-98/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 559639
R;Bossart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S.
R;Bossart-Whitaker, P.; Chang, C.Y.Y.; Novotny, J.; Benjamin, D.C.; Sheriff, S.
A;Title: The crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibody NIO-staphylococcal nuclease complex at in the crystal structure of the antibodylococcal nuclease of the antibodylococcal nuclease of the antibodylococcal nuclease nuclear nuclear nuclear nuclease nuclear nuclease nuclear nuc
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Pred. No. 0.029;
2; Mismatches (
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Best Local Similarity 81.8%;
Matches 9; Conservative ;
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26 GYSITRGYNWN 36
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Search completed: April 25, 2006, 06:26:10 Job time : 11.3396 secs
GYSITSGYSWN 11
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A Molecule type: mRNA
A, Residues: 1-121 <FIS>
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C Species was musculus (house mouse)
C Species was musculus (house mouse)
C Jate: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999
C Jate: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999
C JACCESSION: S36379
R JANCELL, K.H.
Submitted to the EMBL Data Library, April 1993
A; Reference number: S36376
A; Reference number: S36376
A; Reference number: S36376
A; Residues: 1-59 < ANS
A; Residues: 1-59 < ANS
A; Residues: 1-59 < ANS
A; Rettleborcough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Bur. J. Immunol. 23, 206-211, 1993
A; Rettleborcough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Bur. J. Immunol. 23, 206-211, 1993
A; Reference number: S33394
A; Reference number: S33394
A; Molecule type: MRNA
A; Residues: 1-31,33-39 < KET>
A; Rossidues: 1-31,33-39 < KET>
A; Rossidues: 1-31,33-39 < KET>
A; Residues: 1-
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C; Species: Mus musculus (house mouse)
C; Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C; Accession: 128195
R; Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A; Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A; Faference number: A28195; MulD:88153717; PMID:3267217
A; Recession: 128195
A; Rolecule type: mRNA
A; Residues: 1-117 < SHB>
A; Molecule type: mRNA
A; Residues: 1-117 < SHB>
A; Coss references: UNIPARC:UPI0000114D72; GB:M19775; NID:g195526; FIDN:AAA38343.1; PID:A; MulD:Barfamily: immunoglobulin homology
C; Roywords: heterotetramer; immunoglobulin homology
C; Roywords: heterotetramer; immunoglobulin homology < IMM>
                                    ם
                                A;Cross-references: UNIPARC:UPI0000117542; EMBL:X76018; NID:g416102; PIDN:CAA53605.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <!MM>
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                                                                                                                                                                                                                  Length 116
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Pred. No. 0.035;
0; Mismatches 2; Indels
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                                                                                                                                                                                                          84.4%; Score 54; DB 2;
81.8%; Pred. No. 0.048;
ive 1; Mismatches
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81.8%;
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C,Accession: F25114

R;01lier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.

EMBO J. 4, 3681-3689, 1985

A;Title: The idiotypic network and the internal image: possible regulation of a germ-lin A;Reference number: A91028; MUID:86136012; PMID:3937730

A;Accession: P25114

A;Accession: P25114

A;Residues: 1-115 < OLL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross=references. UNIPARC:UP10000115D28; GB:X03379; NID:g52013; PIDN:CAA27101.1; PID:gC;Superfamily: immunoglobulin V region; immunoglobulin homology C;Superfamily: immunoglobulin V region; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S37200
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: S37200
                                                                                                                                                       Ig heavy chain V region (HP12) - mouse
C,Species: Mus musculus (house mouse)
C,Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
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              GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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HV46_MOUSE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Butheria, Buarchontoglires, Glires, Rodentia, Sclurognathl;
Muroidea; Muridae; Murinae; Mus.
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MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
Levy NS., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during primary immune response.";
primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
J. Exp. Med. 169:2007-2019(1989).
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01-NOV-1990 (Rel. 16, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V region 1B43 precursor.
Mus musculus (Mouse)
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               GBR018 MOUSE
CPAH MOUSE
CPAH MOUSE
Q77279 MYCDU
P95261 MYCTU
Q4HW71 G1BZB
Q4KDS1 PSEP5
Q54W71 G1BZB
Q4KDS1 PSEP5
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03378; CAA27096.1; -; mRNA.
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98 AA; 11202 MW; 4049CF8C7EE8AAE0 CRC64;
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13-5EP-2005 (TrEMBLrel. 31, Last sequence update)
13-5EP-2005 (TrEMBLrel. 31, Last annotation update)
14-segion (Fragment).
Mus musculus (Mouse).
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01-NOV-1990 (Rel. 16, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Mus musculus (Mouse).
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nes 10; Conserv
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HV60 MOUSE
ID HV60 MOUSE
AC P1851;
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NON TER
SEQUENCE
                                                                                                                                                                                                              STRAND
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053VQ4 MOUSE
DC 353VQ4 MOUSE
DT 13-SEP-20
DT 13-SEP-20
DE VH region
OC Bukaryote
OC Mammalia
OC Mammalia
OC MATER
RA Ollier P
RY MEDLINE
RA OLLEOTII
RY MEDLINE
RY A GOUGECEA
RY SUMMITTER
R
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDINE-89279149; PubMed-2499654; DOI=10.1084/jem.169.6.2007;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86136012; PubMed=3937730; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.; The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system."; EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                     PIR; JT0509; HVMS31.

PDB; 1EZV; X-ray; X=22-116.

SMR; P18531; 19-116.

Ensembl; ENSMUSGO0000057048; Mus musculus.

InterPro; IPR007110; Ig-1ike.

InterPro; IPR003596; Ig_v.

SMART; SM00406; IGv. 1.

PROSTIR; PS50835; IG LIKE; 1.

3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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Complementarity-determining-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13095 MW; 4562E03E53DC9E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 119
119 AA; 13931 MW; 502B51A5213F056B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-5EP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-D-JH region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 1;
Pred. No. 0.063;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 AA.
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NON TER 119 119
SEQÜENCE 119 AA; 13931 MW; 502
                                                                             primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
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NUCLEOTIDE SEQUENCE OF 28-29.
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Q53VQ5;
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Matches 10; Conservative
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116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINB=74170779; PubMed=4524622; Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.; Anino-acid sequence of the variable region of the heavy (alpha) chain of a mouse myeloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
                                                                                                                                                                                                                                                                                              MEDLINE=89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8; Rinfret A., Horne C., Dorrington K.J., Klein M.; Rinfret A., Horne C., Dorrington K.J., Klein M.; Requencing and expression of the rearranged MOPC 315 VH gene segment.";
                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus
                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE OF 1-21.
MEDLINE=79148758; PubMed=428562;
Schechter I., Wolf O., Zemell R., Burstein Y.;
"Structure and function of immunoglobulin genes and precursors.";
Fed. Proc. 38:1839-1845(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECURNCE REVISION TO 53.

MEDLINE=77244979; PubMed=268248;
MEDLINE=77244979; PubMed=268248;
Mod Li, Margolies M.N., Givol D., Zakut R.;
Unpublished results, cited by:
Padlan B.A., Davies D.R., Pecht I., Givol D., Wright C.;
Cold Spring Harb. Symp. Vaunt. Biol. 41:627-637(1977).
-!- MISCELLANGOUS: This alpha chain was isolated from a myeloma protein that has anti-dinitrophenyl activity.
                                                                                                                                                                                                                                                                                                                                                                                               Jilka R.L., Pestka S.; "Anino acid sequence of the precursor region of MOPC-315 mouse immunoglobulin heavy chain."; Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
                               ö
      Score 58; DB 2; Length 119;
Pred. No. 0.065;
                               1; Indels
                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-May chain V region MOPC 315 precursor.
Mus musculus (Mouse)
                                                                                                                                        137 AA
                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSMUSGO0000057048; Mus musculus.
Interpro; IPR007110; Ig-like.
Interpro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M27638; AAA61337.1; -; Genomic_DNA
EMBL; X07880; CAA30727.1; -; Genomic_DNA
                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 1-31.
MEDLINE=78094475; PubMed=414225;
                                                                                                                                                                                                                                                                                                                                                   Mol. Immunol. 26:431-434(1989)
          90.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN SEQUENCE OF 19-136.
Query Match
Best Local Similarity 90.9
....hes 10; Conservative
                                                                                                                                        STANDARD;
                                                       1 GYSITSGYSWN 11
                                                                          26 GYSITSGYYWN 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; PL0102; AVMS35.
HSSP; P01820; 1G7J.
SMR; P01822; 20-137
                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                        HV46 MOUSE
P01822;
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                                                                                                                             MOUSE
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R. SITESURE-Mammary tumor. WAP-TGF alpha model. 7 months old;

R. TISSURE-Mammary tumor. WAP-TGF alpha model. 7 months old;

R. TISSURE-Mammary tumor. WAP-TGF alpha model. 1.073/pnas.242603899;

R. Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

R. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B. Astapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Forenge C.,

R. Aras S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Antilon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

R. Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

R. Butkerifeld Y.S.W., Touchman J.W., Green B.D., Dickson M.C.,

R. Butkerifeld Y.S.W., Krzywinski M.I., Skalaka U., Smallus D.B.,

R. Generation and initial analysis of more than 15,000 full-length human mouse colbn sequences."

T. Tand mouse colbn sequences."
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                                                                                                                          Ig heavy chain V region MOPC 315. Pramework-1.
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Framework-4.
By similarity.
G -> GG (in Ref. 1; CAA30727).
G -> H (in Ref. 2).
G -> H (in Ref. 4).
N -> D (in Ref. 4).
Missing (in Ref. 4).
                                                                                                                                                                               Complementarity-determining-1.
                                                                                                                                                                                                                                  Complementarity-determining-2. Framework-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Last annotation update)
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                                               Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 AA
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
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STRAIN=Mix FVB/N;
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Name=LOC238447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 10; Conserv
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region (Fragment)
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic) antibodies in the GAT system.";
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                                                                                                                                                                                                                                                                                                                                       90.6%; Score 58; DB 2; Length 479; 90.9%; Pred. No. 0.29;
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Pred. No. 0.11;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                1; Indels
  IISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                      NIH MGC Project;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03375, CAA27078.1; -; mRNA.
EMBL; X03374; CAA27072.1; -; mRNA.
                                                                                                                                                                                                                                                                                  Immunoglobulin domain.
SEQUENCE 479 AA, 51992 MW; 768E39A138918892 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH-region (Fragment)
Mus musculus (Mouse)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                   SUBLICATOR (VAN-SOUT) TO THE PRIBLY GENERALLY BENEL) BC002091; AAH02091.1; -; MRNA. HSSP; P01820; 1G7J.

GO, GO:0003823; F:antigen binding; IEA. GO:0003823; F:antigen binding; IEA. InterPro; IPR003199; Ig_C1.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF07654; C1-8et; Z.
SWART; SW00406; Ig_V.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00299; IG_MHC; UNKNOWN_Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OS3VR6 MOUSE PRELIMINARY;
QS3VR6;
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Q53VR7;
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Best Local Similarity 81...
Best Local 9; Conservative
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nes 10; Conservative
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26 GYSITRGYNWN 36
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CSTRAINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RELIABRE R.L., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

B Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

B Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haidh F.,

B Caralecon M., Soares M.B., Bonaldo M.F., Carannon R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

B Rosak S.A., McEwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodriques S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Koung A.C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Control A. A., Schein J.E., Jones S.J.M., Marra M.A.;

Rodriguez A.C., Garby J. M. Marra M.A.;

Rodriguez A.C., Garby J. M. Marra M.A.;

Rodriguez A.C., Schwilski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Schwilski M.I., Marra M.A.;

Rodriguez A.C., Schwilski M.I., Marra M.A.;
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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                        MEDILINE-86136012; PubMed-3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fougereau M.;
Submitted (NOV-1986)
Submitted (NOV-1986)
Submitted (NOV-1986)
EMBL; X03374; CAA27077.1; -; mENA.
EMBL; X03374; CAA27071.1; -; mENA.
EMBL; X03374; CAA27071.1; -; mENA.
NON TER 1
NON TER 1
SEQÜENCE 120 AA; 13892 MM; 013452306EBBA3BE CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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NUCLEOTIDE SEQUENCE OF 28-29.
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Q5U413;
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NUCLEOTIDE SEQUENCE.
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InterPro; IPR003599; Ig.
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053VQ1 MOU
1D Q53VQ1
AC Q53VQ
DT 13-SE
DT 13-SE
DT 13-SE
DE VH-D-
OC Mamma
OC Mamma
OC Murid
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Marinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.9%; Score 55; DB 2; Length 483; 81.8%; Pred. No. 0.93;
                                                                       EMBL; BCO85312, AM88312.1; -; mRNA.
ENSEMD; ENSWUSGO00054328; Mus musculus.
CO, GO.003823; P.antigen binding; IEA.
InterPro; IPR0031599; Ig.
InterPro; IPR003109; Ig-like.
InterPro; IPR003109; Ig-like.
InterPro; IPR003106; Ig-MrC.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
SMART; SM00409; IG.
SWART; SM00409; IG.
SWART; SM00409; IG.
PROSITE; PSS0835; IG_LIKE; 4.
PROSITE; PSS0835; IG_LIKE; 4.
PROSITE; PSS0835; IG_LIKE; 4.
PROSITE; PSS0839; IG_MHC; UNRXOWN 2.
SRQUENCE 483 AA; $\frac{5}{2}2114 MW; 7C272DA501A4A0D1 CRC64;
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                                                       Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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GO; GO:0003823; F:antigen binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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             STRAIN=FVB/N; TISSUE=Colon;
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Best Local Similarity 81.8
Matches 9; Conservative
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Q56988;
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NIH MGC Project;
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                                       NIH MGC Project;
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0265988 RAT
10-MA
DT 10-MA
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13-SBP-2005 (TrEMBLrel. 31, Last sequence update)
13-SBP-2005 (TrEMBLrel. 31, Last annotation update)
13-SBP-2005 (FrEMBLrel. 31, Last annotation update)
Wh region (Fragment)
Mus musculus (Mouse)
Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Burchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                     82.8%; Score 53; DB 2; Length 590;
81.8%; Pred. No. 2.5;
ive 0; Mismatches 2; Indels
InterPro; IPR007110; Ig-like.
InterPro; IPR003005; Ig_Mc.
InterPro; IPR003005; Ig_Mc.
InterPro; IPR003595; Ig_v.
InterPro; IPR003596; Ig_v.
InterPro; IPR00409; IG_r.
SMART; SM00409; IG_r.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
RPOSITE; PS00299; IG_MRC; UNKNOWN 3.
RPOSITE; PS00299; IG_MRC; UNKNOWN 3.
SRQUENCE 590 AA; 65088 MW; PAC77FFA82302304 CRC64;
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Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03379; CAA27102.1; -; mRNA.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 AA; 11191 MW; B3585BBB6P080616 CRC64;
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Last annotation update)
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OS3VO1 MOUSE PRELIMINARY;
Q53VQ1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q53VQ0 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 81.8 nes 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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Fougereau M.;
Submitted (NOV-1986) to the EMBL/G
EMBL; X03377; CAA27089.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=168;
MEDLINE=97419515; PubMed=9274030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crobiology 143:2769-2774(1997).
                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE OF 28-29.
VH-D-JH region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         005254 BACSU PRELIMINARY;
005254; Q795M0;
01-JUL-1997 (TrEMBLrel. 04
                                                                                                                                                                                                                                                                                                                                      8; Conservative
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                                                     Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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Matches 8; Conserv
                                                                   NCBI_TaxID=10090;
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SEQUENCE
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MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network at the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
                                                     Ollier P., Rocca-Serra J., Somme G., Theze J., Pougereau M.;
"The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sclurognathi;
Muridae; Murinae; Mus.
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Pred. No. 2.6;
1; Mismatches 2; Indels
                                                                                                                                               Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03379; CAA27101.1; -; mRNA.
                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fougereau M.;
Submitted (NOV-1986) to the EMBL/GenBank/DDBJ databases.
EMBL; X03377; CAA27090.1; -; mRNA.
NON_TER
                                                                                                                                                                                                                 115 AA; 13257 MW; D465A5854DF459A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
VH region (Fragment)
Mus musculus (Mouse)
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Last annotation update)
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                                         MEDLINE=86136012; PubMed=3937730;
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Q53VQ9 1
13-SEP-2005 (TEMBLE1 31,
13-SEP-2005 (TEMBLE1 31,
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  NCBI_TaxID=10090;
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DD 13-SE
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ID Q53
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NUCLECTIDE SEQUENCE.
MEDLINE=86136012; PubMed=3937730;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
"The idiotypic network and the internal image: possible regulation of a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
EMBO J. 4:3681-3688(1985).
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Hilbert H., Duesterhoeft A., Pohl T.M., Weltzenegger T.,
"Analysis of the Bacillus subtilis genome: cloning and nucleotide
sequence of a 62 kb region between 275 degrees (rrnB) and 284 degrees
Mus musculús (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98044013; PubMed=9384377; DOI=10.1038/36786; Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolottin A., Borchert S., Borriss R., Boursier L., Brans A., Braum M., Brignall S.C., Bron S., Bornilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Danniel R.A., Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T. Entian K.-D., Errington J., Fabret C., Ferrari B., Foulger D., Fritz C., Pujta M., Pujita Y., Funa S., Galizzi A., Galaer D., Goffeau A., Golightly B.J., Grandi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOV-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 AA; 13844 MW; 6B1BC8C7DC77E147 CRC64;
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01-UL1.1997 (TrEMBLrel. 04, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein yufp.
Name=yufp; OrderedLocusNames=BSU31560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 48; DB 2; 72.7%; Pred. No. 3.2;
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1; Mismatches
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RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,

RA Jones L.-M., Jooria B., Karamaca D., Kasharar Y., Klasar Blanchard M.,

RA Kueln C., Kobayashi Y., Koetter P., Kandnager G., Krooph S.,

Kumano M., Kurita K., Lapidus H., Lardinois S., Lauber J.,

RA Kumano M., Kurita K., Levine A., Liu H., Masuda S., Mauel C.,

RA Gazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,

RA Gazarevic V., Lee S.-M., Levine A., Liu H.,

Roback M., Noone D., O'Reilly M., Ogdwar A., Oudega B.,

RA RAF S.-H., Parro V., Pohl T.-M., Portetelle D., Porwollik S.,

RA Ray M., Reynolids S., Rieger M., Rivolta C., Rocha B., Rapoport G.,

RA Rescott A.M., Presecan B., Pujic P., Purnelle B., Rapoport G.,

RA Rose M., Sadale Y., Sato T., Sakowska A., Seror S.-J., Serror P.,

RA Rose M., Sadale Y., Sato T., Sakowska A., Seror S.-J., Serror P.,

RA Rose M., Sadale Y., Sato T., Sakowska A., Seror S.-J., Serror P.,

RA Scoffene F., Selduchi J., Sekowska A., Seror B.,

RA Scoffene F., Selduchi J., Sekowska A., Seror B.,

RA Scoffene F., Selduchi J., Sekowska A., Seror B.,

RA Samott A., Viari A., Wandut R., Yandar T., Terpstra P.,

RA Westarenger T., Winers P., Wippt A., Yamanoto H., Yamane K.,

RA Westarenger T., Winers P., Wippt A., Yamanoto H., Yamane K.,

RA Westarenger T., Winers P., Wippt A., Yamanoto H., Yamane K.,

RA Westarenger T., Winers P., Wippt A., Yamanoto H., Yamane K.,

RA Yoshikawa H., Danchin A.,

RA The complete genome sequence of the Gram-positive bacterium Bacillus B.

REME; 299120; Calbisia P., Genomic_DNA.

RIK; E70009; E70009; R. Calbisia J., F., Genomic_DNA.

RIK; E70009; E70009; R. Calbisia J., F., Genomic_DNA.

RIK; R. Processis Frienansport: IRA.

Col, Go:0006210; R. Freansport: IRA.

Col, Go:0006212; Resensport: IRA.

Collecter Processis Repense M.,

Refer Loccome; Hypothetical protein.

RA Complete proteome; Hypothetical protein.

Refer Loccol Similarity 634; Rescented Beet Loccol
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Search completed: April 25, 2006, 06:24:35 Job time : 61.7358 secs

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RESULT 1
US-08-887-352B-11
Appl
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                                                                                                                                    April 25, 2006, 06:25:05; Search time 14.8396 Seconds (without alignments) 61.284 Million cell updates/sec
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                  GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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(cgn2_6/ptodata/1/laa/5_COMB.pep:*
(cgn2_6/ptodata/1/laa/6_COMB.pep:*
(cgn2_6/ptodata/1/laa/H_COMB.pep:*)
(cgn2_6/ptodata/1/laa/PGTUS_COMB.pep:*)
(cgn2_6/ptodata/1/laa/RECOMB.pep:*)
(cgn2_6/ptodata/1/laa/RECOMB.pep:*)
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US-09-296-005-11

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US-09-296-005-12

US-09-290-171-11

US-09-210-171-11

US-09-210-171-12

US-09-216-028-11

US-10-113-996-11

US-10-113-996-11

US-08-10-113-996-12

US-09-109-207C-2

US-09-296-005-3

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US-09-171-3
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                                                                                                                                                                                                                                                                                                                                                               572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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US-US-US-152B-11

US-US-US-152B-11

Sequence 11, Application US/0887352B

Patent No. 599451

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Improving Polypeptides and Method of

TITLE OF INVENTION: Improving Polypeptides

TITLE OF INVENTION: Improving Polypeptides

NUMBER OF SEQUENCES: 26

CORRESPONDENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE Genentech, Inc.

STREET: 1 DNA Way

COUNTRY: USA

ZIP: 94000 E POSM:

MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk

COMPUTER: 1BM PC COMPATION COMPATION TOWN

MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk

COMPUTER: Winbeltin (Genentech)

COMPUTER: Winbeltin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,352B

FILING DATE: 03-JUI-1997

CLASSIFICATION NUMBER: 39,044

REGISTRATION NUMBER: 910-191

TELEPHONE: 550/952-981

INFORMATION POR SEQ ID NO: 11:

SEQUENCE TABARATERISTICS:

INFORMATION POR SEQ ID NO: 11:

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                                         Sequence 21,
Sequence 20,
Sequence 21,
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US-09-802-077-3
US-08-925-179-3
US-08-887-352B-21
US-08-887-352B-21
US-09-109-207C-21
US-09-296-005-21
US-09-296-005-21
US-09-296-005-21
US-09-920-171-21
US-09-920-171-21
US-09-920-171-21
US-09-920-171-21
US-09-920-171-21
US-09-113-996-21
US-10-113-996-21
US-10-113-996-21
US-08-887-352B-25
US-08-887-352B-25
US-08-109-207C-25
                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            j LENGTH: 114 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-3528-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 11, Conservative
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RESULT 2 US-08-887-352B-12

Sequence 2, Sequence 3, Sequence 2, Sequence 3,

Sequence 3, Sequence 3,

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Sequence 12, Application US/09109207C

Factor 12, Application US/09109207C

Factor 12, Application US/09109207C

GENERAL INFORMATION:

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

CURRENT FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/051,554

PRIOR FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 12

LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09296005

Sequence 11, Application US/09296005

Patent No. 6290957

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides

TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides

FILE REFERENCE: P1123CIr

CURRENT FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 08/887,352

RARLIER FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 11

LENGTH: 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 64; DB 2; Length 114; 100.0%; Pred. No. 0.0043; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-109-207C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Artificial CCATION: 1-114 CTHROMATION: Heavy chain sequence derived from MAE11 (15-09-296-005-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-09-296-005-12
Sequence 12, Application US/09296005
Patent No. 6290957
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                        26 GYSITSGYSWN 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial
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S-09-101-11, Application US/09109207C
Baquence 11, Application US/09109207C
Baquence 11, Application US/09109207C
Batent No. 6172213
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TIPLE OF INVENTION:
TIPLE OF INVENTION:
TIPLE OF INVENTION NUMBER: US/09/109,207C
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT APPLICATION NUMBER: US/09/105,207C
PRIOR PLING DATE: 1999-07-03
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 11
Sequence 12, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Auti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 64; DB 1; Length 114; 100.0%; Pred. No. 0.0043; Live 0; Mismatches 0; Indels
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; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-11
                                                                                                                                                                                                                                                                                                                                            COUNTY:

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,3528
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SVODGA, Craig G.
REGISTRATION NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/225-1489
TELEPHONE: 650/25-1489
TELEPHONE: GOJS5-29881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 114 amino acids
Amino Acid
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Best Local Similarity 100.
Matches 11; Conservative
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ORGANISM: Artificial
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FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT PILING NATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-0-02
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
LENGTH: 14
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                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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ORGANISM: Artificial
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US-09-716-028-12
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            GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gB Antibodies and Method of Improving Polypeptides
TITLE REPRENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER APPLICATION NUMBER: US 08/887,352
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 12
TENDER OF 124
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Sequence 11, Application US/09920171

Sequence 11, Application US/09920171

Patent No. 6682735

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lowan, Henry B.
APPLICANT: Dardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Improved Anti-IgB Antibodies (as amended)
FILE REFERENCE: P1123C20S
FILE REFERENCE: P1123C20S
FRICH PRILING DATE: 2001-08-01
PRIOR PILING DATE: 1997-07-02
PRIOR PILING DATE: 1997-07-02
PRIOR PILING DATE: 1999-04-21
FRIOR PILING DATE: 1999-04-21
FRIOR PILING DATE: 1999-04-21
FRIOR PILING DATE: 1999-04-21
FRIOR FILING DATE: 1999-04-21
FRIOR FILING DATE: 1999-04-21
FRIOR FILING DATE: P199-04-21
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Sequence 12, Application US/09920171

Sequence 12, Application US/09920171

Sequence 12, Application Grant Incomman, Henry B.

APPLICANT: Lowman, Henry B.

APPLICANT: Presta, Leonard G.

APPLICANT: Lowe, John

APPLICANT: Lowe, John

TITLE OF INVENTION: Improved Anti-IgB Antibodies (as amended)
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US-09-920-171-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-296-005-12
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100.0%; Pred. No. 0.0043;
tive 0; Mismatches 0
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Best Local Similarity 100.
Matches 11; Conservative
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US-09-716-028-11
US-09-716-028-11
Sequence 11, Application US/09716028
Patent No. 6723833
Patent No. 6723833
Patent No. 6723833
FITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
PLE REFERENCE: P1123R1
CURRENT PILING DATE: 10509/716,028
CURRENT PILING DATE: 1090-011-17
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 11.
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Sequence 12, Application US/09716028

Parent No. 6723833

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

TITLE REFERENCE: PI123R1

CURRENT APPLICATION NUMBER: US/09/716,028

CURRENT FILING DATE: 2000-11-17
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                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1-114
OTHER INFORMATION: Heavy chain sequence derived from MAB11
; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-09-920-171-12
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09/920,171

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; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09;
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; LENGTH: 114
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100.0%; Score 64; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                     FEATURE:
NAME/KEY: Artificial
LOCATION: 1-114
CHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-716-028-12
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US-10-113-996-11
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'Sequence 12, Application US/10113996
'Patent No. 6761889
'GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Jardieu, Paula M.
APPLICANT: Journand, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies
'FILE REFERENCE: P1123C3US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10113996
Patent No. 6761889
GENERAL INFORMATION:
GAPLICANT: Lowen, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REPERENCE: P1123C3US
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CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: US 08/687,352
PRIOR FILING DATE: 1997-07-02
PRIOR PLING DATE: 1997-07-05
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                          NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                      ORGANISM: Artificial
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                                                        SEQ ID NO 12
LENGTH: 114
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improving Polypeptides

TITLE OF INVENTION: Improving Polypeptides

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

COUNTRY: Coult San Francisco

COUNTRY: USA
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                                                                                                                 Query Match 100.0%; Score 64; DB 2; Length 114; Best Local Similarity 100.0%; Pred. No. 0.0043; Matches 11; Conservative 0; Mismatches 0; Indels
                                        ; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-10-113-996-12
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/897,352B

FILING DATE: 03-Jul-1997

CLASSIFICATION: 5:0

ATTORNEY/AGENT INFORMATION:

NAME: SYODOGA, Craig G.

REGISTRATION NUMBER: 99,044

REGISTRATION NUMBER: P1123

TELECOMMUNICATION:
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US-08-887-352B-3
; Sequence 3, Application US/08887352B
; Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/08887352B
; Patent No. 5994511
ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
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US-08-887-352B-2
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Sequence 2, Application US/09109207C

Patent No. 6172213

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of Improving Polypeptide
FILE REPERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT PILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44

SEQ ID NO 2
LENGTH: 121
GENERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DAN WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPTER: BARDABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPTER: The PC compatible
COMPTER: The PC compatible
COMPTER: Sylvent PC-DOS/MS-DOS
SOFTWARE: O3-JUL-1997
CURRENT APPLICATION NUMBER: US/08/087,352B
FILING DATE: 03-JUL-1997
CURRENT APPLICATION NUMBER: P1123
TELEROMMUNICATION INFORMATION:
NAME: Sycboda, Craig G.
TELEROMMUNICATION INFORMATION:
TYPE: AMINO Acid
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100.0%; Pred. No. 0.0045;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 11; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 11; Conservative
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US-09-109-207C-2
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US-09-109-207C-2
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Sequence:

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Run

Scoring table:

Searched:

Minimum DB (Maximum DB)

Database :

Result

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Sequence 19, Application US/10764428

Publication No. US20040229310A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WETHODS FOR PRODUCING HUMANIZED ANTIBODIES AND IMPROVING TITLE OF INVENTION: CULTURE TITLE OF INVENTION: CULTURE TITLE OF INVENTION: VIELD OF ANTIBODIES OR ANTIGEN BINDING FRAGMENTS IN CELL TITLE REPRENCE: 11669-1200501

FILE REPRENCE: 11669-1200501

CURRENT PLING DATE: 2004-01-23

CURRENT FILING DATE: 2004-01-23

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PARENTIN VEFSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 11, Application US/09920171; Sequence 11, Application US/09920171; Patent No. US20020054878A1; GRNERAL INFORMATION:
; GRNERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Jardieu, Paula M.
; TILB OF INVENTION: Improved Anti-IgB Antibodies (as amended); TILB REFERENCE: P1123CUS; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR PILING DATE: 1999-04-21
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Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels
US-09-920-171-25
US-09-920-171-26
US-10-113-996-25
US-10-113-996-25
US-10-791-619-25
US-10-791-619-25
US-10-698-073-19
US-09-920-171-22
US-09-920-171-23
US-10-113-996-23
US-10-113-996-23
US-10-113-996-23
US-10-791-619-23
US-10-791-619-23
US-10-698-073-15
US-10-698-073-15
US-10-698-073-11
US-10-698-073-11
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US-10-764-428-19
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ORGANISM: Artificial Sequence
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      GYSITSGYSWN 11
        RESULT 2
US-09-920-171-11
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LENGTH: 11
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118, Appl
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                                                                                                                                                April 25, 2006, 06:58:17; Search time 47.9434 Seconds (without alignments) 95.866 Million cell updates/sec
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Sequence 4, A
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
1: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
                               GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-113-996-11
US-10-791-619-12
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US-10-791-619-12
US-10-791-619-12
US-09-920-171-3
US-09-920-171-3
US-10-113-996-2
US-10-113-996-3
US-10-791-619-3
US-09-802-077-3
US-09-802-077-3
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US-10-113-996-20
US-10-113-996-21
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Match Length DB
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                           ORGANISM: Artificial Sequence
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ORGANISM: Artificial
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SEQ ID NO 11
LENGTH: 114
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GENERAL INCOMMATION:
APPLICANT: LOWARTHON:
APPLICANT: Presta, Leonard G.
APPLICANT: Jordeu, Paula M.
APPLICANT: Jordeu, Paula M.
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: 19123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1999-04-21
FRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 12
LENGTH: 114
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                                                                                                                                                                                     Query Match 100.0%; Score 64; DB 3; Length 114; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                        FEATURE:
; CTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-05-920-171-12
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APPLICANT: Presta, Leonard G.
APPLICANT: Presta, Leonard G.
APPLICANT: Joadieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REFERENCE: P123333
FILE REFERENCE: P133334
CURRENT APPLICATION NUMBER: US 010/113,996
CURRENT APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 44
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Publication No. US20030149244A1
GENERAL INFORMATION:
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Patent No. US20020054878A1
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                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11, Conservative
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      NUMBER OF SEQ ID NOS: 44
SEQ ID NO 11
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PREDICTARY: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides FILE REPRENCE: P1123R1
CURRENT APPLICATION NUMBER: US/10/791,619
CURRENT PILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/109,207
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NOS: 44
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                                                                                                      Query Match
100.0%; Score 64; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels
FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11 US-10-113-996-11
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US-10-113-996-12
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Dardieu, Paula M.
; TILLS OF INVENTION: Improved Anti-IgE Antibodies
; TILE REFERENCE: P1123G3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 1299-04-01
; PRIOR PILING DATE: 1299-04-02
; PRIOR FILING DATE: 1999-04-21
; PRIOR PPLICATION NUMBER: US 09/296,005
; PRIOR PLING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/206,171
; PRIOR SEQ ID NOS: 44
; SEQ ID NO 12.
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APPLICANT: BALL, HOWARD A.

TITLE OF INVENTION: COMBINATION OF DEHYDRORPIANDROSTERONB OR

TITLE OF INVENTION: DEHYDROSPERONB-SULFATE WITH AN ANTI-IGE

TITLE OF INVENTION: DEHYDROSPERONB-SULFATE WITH AN ANTI-IGE

TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: PULMONARY DISEASE

TITLE OF INVENTION: PULMONARY DISEASE

TITLE OF INVENTION: DEMAN TO 10/699,073

CURRENT APPLICATION NUMBER: US/10/699,073

CURRENT PILING DATE: 2003-10-26

PRIOR PILING DATE: 2003-07-31

NUMBER OF SEQ ID NOS: 19

SOFTHMARE: PATENTION VET: 3.2

SOFTHMARE: PATENTION VET: 3.2

LENGTH: 114
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US-10-698-073-5
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; Patent No. US20020054878A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Jardieu, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
FILE REFERENCE: P1123C2US
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Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                               Query March 100.0%; Score 64; DB 5; Length 114; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 11; Conservative 0; Mismatches 0; Indels
; OTHER INFORMATION: Humanized Monoclonal Antibody
US-10-698-073-4
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CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-07-05
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10698073 Publication No. US20050026881A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROBINSON, CYNTHIA B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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US-09-920-171-2
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| Sequence 12, Application US/10791619
| Publication No. US20040259077A1
| Publication No. US20040259077A1
| Publication No. US20040259077A1
| GENERAL INPORMATION:
| APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
| TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
| TITLE OF INVENTION: UNDORSE: US/04-03-02
| CURRENT PEDILCATION NUMBER: US/04/109,207
| PRIOR FILING DATE: 1998-06-30
| NUMBER OF SEQ ID NOS: 44
| TYPE: PRI
| TYPE: PRI
| TYPE: PRI
| TYPE: PRI
| PROGRANSE: Artificial
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; Sequence 4, Application US/200502681A1
; Bellication No. US2005002681A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE SULFATE WITH AN ANTI-1GR
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: WIDMERR: US/10/698,073
; CURRENT PILING DATE: 2003-10-26
; PRIOR PILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTHARE: Patentin Ver. 3.2
; SEQ ID NO 4

LENGTH: 114
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                                                                                                                                                                      100.0%; Score 64; DB 5; Length 114; 100.0%; Pred. No. 0.011; tive 0; Mismatches 0; Indels
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; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-791-619-12
                                NAME/KRY: Artificial
LOCATION: 1-114

CTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-791-619-11
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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LOCATION: 1-114
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                             Gapa
                                                                                                                                                                                                                                                                        Sequence 3. Application US/09920171
; Sequence 3. Application US/09920171
; Patent No. US20020054878A1
; GARREAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Leowe, John Improved Anti-IgR Antibodies (as amended)
FILE REPERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT PILING DATE: 1097-01
PRIOR PILING DATE: 1997-07-02
PRIOR PILING DATE: 1997-04-21
PRIOR PLILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 3
LENGTH: 121
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Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels
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Publication No. US20030149244A1
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Lowmen, Henry B.
APPLICANT: Dardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
TILLE REFERENCE: P1123C3US
CURRENT APPLICATION NUMBER: US/10/113,996
CURRENT APPLICATION NUMBER: US 09/887,352
PRIOR APPLICATION NUMBER: US 09/296,005
PRIOR PILING DATE: 1997-07-02
PRIOR PILING DATE: 1999-04-21
PRIOR PLLING DATE: 1999-04-21
PRIOR FILING DATE: 1990-04-21
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US-10-113-996-2
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US-10-113-996-2
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of Improving Polypeptides FILE REPERENCE: Pli2RI CURRENT APPLICATION NUMBER: US/10/791,619
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/109,207
PRIOR PILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: F(ab) sequence derived from MAE11
                                                                                                      APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Dresta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REFERENCE: P112333US
CURRENT APPLICATION NUMBER: US/10/113,996
CURRENT FILING DATE: 2002-04-01
PRIOR PILING DATE: 1999-04-21
PRIOR PILING DATE: 1999-04-21
PRIOR PILING DATE: 1999-04-21
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
SROID NOS: 44
SROID NOS: 44
LENGTH: 121
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US-10-791-619-2
, Sequence 2, Application US/10791619
; Publication No. US20040259077A1
; GENERAL INFORMATION:
US-10-113-996-3
; Sequence 3, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
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US-10-791-619-3
Sequence 3, Application US/10791619
Sequence 3, Application US/10791619
Sequence 3, Application No. US20040259077A1
GENERAL INFORMATION: Bloomand, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE REFERENCE: P1123B1
CURRENT APPLICATION WUMBER: US/10/791,619
CURRENT APPLICATION WUMBER: US/09/109,207
PRIOR APPLICATION WUMBER: US/09/109,207
PRIOR APPLICATION WUMBER: US/09/109,207
PRIOR PELING DATE: 1989-06-30
PRIOR PLING DATE: 1997-07-03
MUMBER OF SEQ ID NOS: 44
PRIOR PLING DATE: 1997-07-03
MUMBER OF SEQ ID NOS: 44
PRIOR PLING DATE: 1997-07-03
MUMBER OF SEQ ID NOS: 44
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1: /SIDS5/ptodate/1/pubpaa/US06 NEW FUB.pep:*

2: /SIDS5/ptodata/1/pubpaa/US06 NEW FUB.pep:*

3: /SIDS5/ptodata/1/pubpaa/US07 NEW FUB.pep:*

4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_FUB.pep:*

5: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*

7: /SIDS5/ptodata/1/pubpaa/US10_NEW_FUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US11 NEW_FUB.pep:*

8: /SIDS5/ptodata/1/pubpaa/US11 NEW_FUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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64
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl	Appl	ppli	Appli	Appl	\ppli	\ppli	Appl																	
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Description	Sequence	Sequence	Sequence			Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence
αı	US-11-084-554-10	US-11-136-250-10	US-10-923-327-4	US-10-923-327-5	US-11-208-422-48	US-11-208-422-50	US-11-208-422-52	US-10-923-327-13	US-10-923-327-14	US-10-923-327-18	US-10-923-327-19	ᅻ	US-10-923-327-9	US-10-923-327-11	US-11-208-422-20	US-11-208-422-21	US-11-208-422-22	US-11-012-353-70	US-10-512-184-34	US-10-512-184-71	US-10-512-184-49	US-11-009-939-22	US-11-012-353-69	US-11-012-353-75	US-11-012-353-79
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Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.6	90.6	90.6	90.6	85.9	84.4	84.4	84.4
Score	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	28	58	28	58	55	24	54	24
Result No.	-	74	m	4	S	ø	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Sequence 12, Appl Sequence 12, Appl Sequence 52, Appl Sequence 77, Appl	81, 16, 16, 83,	74, 73, 44, 162,	Sequence 34, Appl Sequence 36, Appl Sequence 38, Appl Sequence 40, Appl Sequence 1548, Ap
US-10-946-836A-12 US-10-988-207-12 US-11-012-353-52 US-11-012-353-77		44444	US-10-469-469-34 US-10-469-469-36 US-10-469-469-38 US-10-469-469-40 US-11-054-515-1548 US-11-266-444-1548
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ALIGNMENTS

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US-11-084-554-10

US-11-084-554-10

Sequence 10, Application US/11084554

Publication No. US5050260679A1

GENERAL INFORMATION:

APPLICANT: Kelleram, Sirid-Ai

APPLICANT: Kelleram, Sirid-Ai

APPLICANT: Kelleram, Sirid-Ai

APPLICANT: Korver; Wouter

TILE OF INVENTION: ANTIBODIES THROUGH V GENB MANIPULATION

FILE REFRENCE: ADSENTALION OF STATE CONSTRUCTION OF STATE CONSTRUCT
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TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE TITLE OF INVENTION: PULMONARY DISEASE FILE REFERENCE: 30775-723.501
CURRENT APPLICATION NUMBER: US/10/923,327
CURRENT FILING DATE: 2004-08-20
PRIOR PLING DATE: 2004-08-20
PRIOR PLING DATE: 2003-10-29
PRIOR FLING DATE: 2003-10-29
PRIOR FILING DATE: 2003-07-31
NUMBER OF SQOTOMBER: 60/492,231
SRO ID NOS: 19
SOFTWARE: PATENTIN Ver. 3.3
SRO ID NO S: 3
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Sequence 48, Application US/11208422
Sequence 48, Application US/11208422
Publication No. US20060067930A1
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Lowman, Henry B.
APPLICANT: Lowman, Henry B.
APPLICANT: Marvin, Jonathan S.
APPLICANT: Marvin, UsorPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
FILE REPERENCE: P2158R1
CURRENT FILING DATE: 2005-08-19
CURRENT FILING DATE: 2005-08-19
PRIOR PILING DATE: 2004-08-19
PRIOR FILING DATE: 2004-08-19
SEQ ID NOS: 54
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 64; DB 6; Length 114; 100.0%; Pred. No. 0.0014;
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Best Local Similarity 100.0%; Score 64; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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APPLICANT: Lien, Samantha APPLICANT: Lien, Samantha APPLICANT: Lowman, Henry B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
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Best Local Similarity
Matches 11; Conserva
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| Sequence 4, Application US/10923327
| Sequence 4, Application US20050261208A1
| GENERAL INFORMATION:
| APPLICANT: ROBINSON, CYNTHIA B. |
| APPLICANT: ROBINSON, CYNTHIA B. |
| TITLE OF INVENTION: DEHYDROEPIRANDROSTERONB OR TITLE OF INVENTION: DEHYDROEPIRANDROSTERONB SULPATE WITH AN ANTI-IGE |
| TITLE OF INVENTION: DEHYDROEPIRANDROSTERONB OR TITLE OF INVENTION: DULMONARY DISEASE |
| TITLE OF INVENTION: DULMONARY DISEASE |
| TITLE OF INVENTION: PULMONARY DISEASE |
| FILE REFERENCE: 30775-73.501 |
| CURRENT APPLICATION NUMBER: US/10/923,327 |
| CURRENT PILING DATE: 2004-07-30 |
| PRIOR PILING DATE: 2004-07-30 |
| PRIOR PILING DATE: 2003-07-31 |
| NUMBER OF SEQ ID NOS: 19 |
| SOFTWARE: PatentIN Ver. 3.3 |
| SEQ ID NO 4 |
| LEARTH: 114
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Sequence 5, Application US/10923327

Sequence 5, Application US/10923327

Sequence 5, Application Os. US20050261208A1

SEMENAL INFORMATION:

APPLICANT: BALL, HOWARD B.

TITLE OF INVENTION: COMBINATION OF DEHYDROSFIENONE OR

TITLE OF INVENTION: DEHYDROSFIENONE-SULFATE WITH AN ANTI-IGE
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100.0%; Score 64; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Length 98;
                                                                                                                                                                                                                                                                                                                                                               Score 64; DB 7; Lengtn >v. Pred. No. 0.0012;
               PRIOR FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: PCT/US2005/009306
PRIOR FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: 60/574,661
PRIOR FILING DATE: 2004-05-24
PRIOR FILING DATE: 2004-05-24
PRIOR FILING DATE: 2004-01-19
NUMBER OF SEQ ID NOS: 266
SOFTWARE: PRAESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 10
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Best Local Similarity 100.º
Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-11-136-250-10
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CURRENT FILING DATE: 2004-08-20
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US-10-923-327-18
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Sequence 13, Application US/10923327
Sequence 13, Application US/10923327
Sequence 13, Application US/10923327
Sequence 13, Application US/10923327
GENERAL INFORMATION:
APPLICANT: BALL, HOWARD A.
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE SULPATE WITH AN ANTI-IGE
TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: AUTHONARY DISEASE
TITLE REFERENCE: 30775-723.501
CURRENT APPLICATION NUMBER: US/10/923,327
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; Sequence 52, Application No. US20060067930A1
; Bublication No. US20060067930A1
; GENERAL INFORMATION:
    APPLICANT: Adams, Camellia W.
    APPLICANT: Lien, Samantha
; APPLICANT: Marvin, Jonathan S.
    APPLICANT: Marvin, Jonathan S.
    APPLICANT: Marvin, Jonathan S.
    APPLICANT: Marvin, Jonathan S.
    APPLICANT: Weng, Yu-Ju G.
    TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
    PILE REFERENCE: P2158N1
    CURRENT PRILING DATE: 2005-08-19
    PRIOR PILING DATE: 2004-08-19
    NUMBER OF SEQ ID NOS: 54

APPLICANT: Marvin, Jonathan S.
APPLICANT: Meng, Yu-Ju G.
TITLE OF INVENTION: POLYPEPTIDE VARIANTS WITH ALTERED EFFECTOR FUNCTION
FILE REPREBRIES: P2158H.
CURRENT APPLICATION NUMBER: US/11/208,422
CURRENT FILING DATE: 2005-08-19
PRIOR APPLICATION NUMBER: US 60/603,057
PRIOR PLING DATE: 2004-08-19
NUMBER OF SEQ ID NOS: 54
SEQ ID NO SO
LENGTH: 121
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100.0%; Score 64; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 121;
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100.0%; Pred. No. 0.0014;
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Best Local Similarity 100.
Matches 11; Conservative
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LENGTH: 121
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publication No. US20050261208A1

| Sequence 14, Application US/10923327
| Publication No. US20050261208A1
| GENERAL INPORMATION:
| APPLICANT: ROBINSON, CTNTHIA B. |
| APPLICANT: BALL, HOWARD A. |
| TITLE OF INVENTION: COMBINATION OF DEHYDROSPIANDROSTERONE OR TITLE OF INVENTION: DEHYDROSPIANDROSTERONE OR TITLE OF INVENTION: DILMONARY DISEASE |
| TITLE OF INVENTION: PULMONARY DISEASE |
| FILE REPRESENCE: 30775-733.501 |
| CURRENT APPLICATION NUMBER: PCT/US04/25054 |
| PRIOR FILING DATE: 2004-07-30 |
| PRIOR FILING DATE: 2003-07-31 |
| PRIOR FILING DATE: 2003-07-31 |
| NUMBER OF SEQ ID NOS: 19 |
| SOFTWARE: PLENTING DATE: 2003-07-31 |

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US-10-923-327-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: CONStruct
US-10-923-327-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 64; DB 6; Length 229; 100.0%; Pred. No. 0.0026; Live 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/US04/25054
PRIOR FILING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: 10/698,073
PRIOR APPLICATION NUMBER: 60/492,231
PRIOR FILING DATE: 2003-10-29
PRIOR FILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 3.3
LENGTH: 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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BALL, HOWARD A

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APPLICANT: ROBINSON, CYNTHIA B.
APPLICANT: ROBINSON, CYNTHIA B.
APPLICANT: BALL, HOWARD A.
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: PULMONRAY DISEASE
TITLE OF INVENTION: FOLGO-20
CURRENT FILING DATE: 2004-00-20
FRIOR APPLICATION NUMBER: PCT/US04/25054
PRIOR APPLICATION NUMBER: 60/492,231
PRIOR FILING DATE: 2003-10-29
PRIOR FILING DATE: 2003-10-29
PRIOR FILING DATE: 2003-07-31
SEQ ID NOS: 19
SEQ ID NOS: 19
SEQ ID NOS: 19
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APPLICANT: ROBINSON, CYNTHIA B.
APPLICANT: RALL, HOWARD A.
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: DEHYDRARY DISEASE
FILE REFERENCE: 30775-723.501
CURRENT APPLICATION NUMBER: 105/923,327
CURRENT PILING DATE: 2004-09-20
FRIOR PILING DATE: 2004-07-30
FRIOR PILING DATE: 2004-07-30
FRIOR PILING DATE: 2003-07-31
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CRGANISM: Artificial Sequence
CRATURE:
COTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: CONStruct
US-10-923-327-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: construct
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                                                                                       Sequence 7, Application US/10923327
Publication No. US20050261208A1
GENERAL INFORMATION:
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i, Sequence 9, Application US/10923327
i, Publication No. US20050261208A1
i, GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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GEQUENCE 19, Application US/10923327

Sequence 19, Application US/10923327

Sequence 19, Application US/10923327

PUBLICANT: NO. US2000501208A1

APPLICANT: ROBINSON, CYNTHIA B.

APPLICANT: BALL, HOWARD A.

TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR

TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE

FILE REFERENCE: 30775-723.501

CURRENT APPLICATION NUMBER: US/10/923,327

CURRENT FILING DATE: 2004-07-30

PRIOR PELING DATE: 2004-07-30

PRIOR APPLICATION NUMBER: 60/492,231

PRIOR PELING DATE: 2003-07-31

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PALENTIN VEV. 3.3

LENGTH: 233

LENGTH: 233
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: ANTIHODY FOR TREATMENT OF ASTHWA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: PULMONARY DISEASE
FILE REFERENCE: 30775-723.501
CURRENT FILING DATE: 2004-08-20
CURRENT APPLICATION NUMBER: US/10/923,327
CURRENT APPLICATION NUMBER: PCT/US04/25054
PRIOR FILING DATE: 2004-08-20
PRIOR FILING DATE: 2003-10-29
PRIOR PRIOR FILING DATE: 2003-10-29
PRIOR FILING DATE: 2003-10-29
PRIOR FILING DATE: 2003-10-29
PRIOR FILING DATE: 2003-10-29
PRIOR FILING DATE: 2003-10-29
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100.0%; Score 64; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 11; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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| Sequence 11. Application US/10923327
| Sequence 11. Application No. US2005026120841
| GENERAL INFORMATION:
| Publication No. US2005026120841
| GENERAL INFORMATION:
| APPLICANT: ROBINSON, CTNTHIA B. |
| APPLICANT: ROBINSON, CTNTHIA B. |
| TITLE OF INVENTION: DEHYDROEPLANDROSTERONE OR TITLE OF INVENTION: DHYDRORPLANDROSTERONE SULFATE WITH AN ANTI-IGE |
| TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE |
| TITLE OF INVENTION: PULMONARY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE |
| TITLE OF INVENTION: PULMONARY FOR 110/923, 327 |
| CURRENT FILING DATE: 2004-08-20 |
| PRIOR PILING DATE: 2004-08-20 |
| PRIOR APPLICATION NUMBER: 60/492,231 |
| PRIOR PILING DATE: 2003-10-29 |
| PRIOR PILING DATE: 2003-07-31 |
| NUMBER OF SEQ ID NOS: 19 |
| SEQ ID NO 11 |
| TYPE: PRI TYPE
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US-11-208-422-20
is Sequence 20, Application US/11208422
is Publication No. US20060067930A1
is GENERAL INFORMATION:
is APPLICANT: Adams, Camellia W.
is APPLICANT: Lien, Samantha B.
is APPLICANT: Lien, Gamanthan S.
is APPLICANT: Maryin, Jonathan S.
is TITLE OF INVENTION: POLYEPFILE VALUE OF INVENTION: PLING DATE: 2005-08-19
is PRIOR APPLICATION NUMBER: US 60/603,057
is PRIOR PLING DATE: 2004-08-19
is NUMBER OF SEQ ID NOS: 54
is NUMBER OF SEQ ID NOS: 54
is LENGTH: 451
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US-10-923-327-11
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100.0%; Score 64; DB 6; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels
Best Local Similarity 100.0%; Fred. No. 0.0047; Matches 11; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Sequence is synthesized US-11-208-422-20
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US-10-923-327-11
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Query Match 100.0%; Score 64; DB 7; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ov 1 GYSITSGYSWN 11
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26 GYSITSGYSWN 36

Search completed: April 25, 2006, 07:10:00 Job time : 7.22327 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                   Copyright
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sw model using - protein search, OM protein

April 25, 2006, 06:05:16; Search time 53.3962 Seconds (without alignments) 82.286 Million cell updates/sec Run on:

US-10-764-428-14 58 Title: Perfect

1 GYTFTNYGIN 10 score: Seguence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

A_Geneseq_21:* Database :

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003s:* geneseqp2003s:* geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Add90710 Anti-VEGF		0	m	<u>_</u>	e-	N		•			_				_	Ξ.		•	_	-	Aea40554 Anti-VEGF	Aea40550 Anti-VEGF	Adh62639 Mouse ant
SUMMARIES	10	AD090710	AAW70684	AAW70680	AAB13383	ABP61249	ABP61253	AD014132	ADQ90737	ADQ90732	ADQ90729	ADQ90731	ABR83196	ABR83194	ABR83198	ADU26544	ADU26540	ADU26548	AAW70611	AAG80311	ABP61180	ADR89785	AEA40554	AEA40550	ADH62639
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	* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.3	98.3	98.3	98.3	98.3	98.3	94.8	94.8	94.8	94.8	94.8	94.8	94.8
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ADH62638 ADH62637 ADX58481	ADX58482 ADX58483 AAW24529	AAU80997 AAW24521 AAU80980 AAB84740	AAB84739 AAE27830 AAE27839	AAE27837 AAE27825 AAE27826 AAE27828	AAE27832 AAE27834 ADG67541 ADG67537
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ALIGNMENTS

ADQ90710 standard; peptide; 10 AA (first entry) 21-OCT-2004 ADQ90710; RESULT 1 ADQ90710

Anti-VEGF antibody heavy chain HVR1 peptide SEQ ID NO:14.

antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; entringlammatory; antiangiogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; anti-VEGF antibody; anti vascular endothelial cell growth factor antibody; heavy chain; HVR1.

Homo sapiens. Synthetic.

WO2004065417-A2.

05-AUG-2004.

23-JAN-2004; 2004WO-US001844.

23-JAN-2003; 2003US-0442484P.

(GETH) GENENTECH INC.

Simmons L;

WPI; 2004-562149/54.

Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.

Claim 13; SEQ ID NO 14; 161pp; English

The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid

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with a corresponding HVR1 and/or HVR2 sequence of the variable domain.

The antibody or antigen binding fragment variable domain comprises the modified FR that has improved yield in cell culture compared to an unmodified antibody or antigen binding fragment. The antibody and antigen binding fragment. The antibody and antigen binding fragment The antibody and antigen binding fragment in antibody therapy. The immunomodulatory activities, and can be used in antibody therapy. The producing antibodies or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragment antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and inflammatory, angiogenic and immunological disorders. The present caequence represents a heavy chain HVR1 peptide of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the present invention.
position with a different amino acid, where the different amino acid is the amino acid found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervariable region 1 (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
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Sequence 10 AA;

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100.0%; Score 58; DB 8; Length 10;
100.0%; Pred. No. 0.013;
ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
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RESULT 2

AAW70684 standard; peptide; 118 AA. (first entry) 27-JAN-1999 AAW70684; AAWYO684

IID AAWYO684

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Anti-VEGF humanised antibody variable heavy domain of variant Y0238-3. Heavy variable domain; murine; humanised antibody; anti-vascular endothelial growth factor antibody; anti-VEGF antibody; VEGF-induced angiogenesis; tumour; retinal disorder; age-related macular degeneration; diabetic retinopathy; rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.

Synthetic. в Б

Homo sapiens

W09845331-A2

15-OCT-1998.

98WO-US006604. 03-APR-1998; 97US-00833504. 07-APR-1997; 06-AUG-1997;

(GETH) GENENTECH INC.

New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other angiogenic states, also related nucleic acid, vectors and transformed cells. WPI; 1998-568337/48. Wells JA, Baca M,

Chen YM

Lowman HB,

Presta LG,

Example 3; Fig 10B; 100pp; English

The present sequence represents a variable heavy domain of an affinity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a variable heavy domain of an affinity-matured anti-vascular endothelial growth factor (anti-VBGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VBGF antibody of the invention. The humanised antibodies are used to inhibit VBGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
matured anti-vascular endothelial growth factor (anti-VEGF) antibody variant. The sequence is used in the course of the invention to produce the humanised anti-VEGF antibody of the invention. The humanised antibodies are used to inhibit VEGF-induced angiogenesis, particularly for treating or preventing tumours (of any type) and retinal disorders (e.g. age-related macular degeneration or diabetic retinopathy). They can also be used to treat other conditions that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis, atherosclerosis, Grave's disease, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanised antibody with affinity for vascular endothelial growth factor - for treatment of tumours, retinal disease and other anglogenic states, also related nucleic acid, vectors and transformed cells.
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-VEGF antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-VEGF humanised antibody variable heavy domain of variant Y0192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-vascular endothelial growth factor antibody; anti-VEGF antibo
VEGF-induced anglogenesis; tumour; retinal disorder;
age-related macular degeneration; diabetic retinopathy;
rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
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                                                                                                                                                                                                             100.0%; Score 58; DB 2; Length 118; 100.0%; Pred. No. 0.14; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presta LG, Lowman HB, Chen YM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heavy variable domain; murine; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                          AAW70680 standard; peptide; 118 AA
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97US-00908469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                           1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                              GYTPTNYGIN 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-568337/48.
                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wells JA,
                                                                                                                                                                               Sequence 118 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9845331-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW70680;
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Domain
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                                                                                                                                                                            ABP61249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the heavy chain variable region of the affinity matured anti-vascular endothelial cell growth factor (anti-vEGF) antibody Y0238-3. Humanised F(ab)-12 and affinity matured anti-vEGF antibodies may be used to treat conditions characterised by undesirable excessive necovascularisation. Such conditions include tumours (especially solid ones), rheumatoid arthritis, psoriasis, atheroscierosis, diabetes and other retinopathies, retrolental fibroplasia, age-related macular degeneration, neovascular glaucoma, haemangiomas, thyroid hyperplasia and chronic inflammation. Oedemas associated with tumours, strokes and head trauma, and ascites associated with malignancies, meig's syndrome, hung inflammation, nephrotic syndrome, pericardial effusion and pleural effusion, may also be treated. Monoclonal antibodies are generated in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating edema, tumors, rheumatoid arthritis, psoriasis, atherosclerosis, diabetes and chronic inflammation in a mammal, comprises administering a human vascular endothelial cell growth factor antagonist.
                                                                                                                                                                                                                             antinniammatory; cerebroprotective; cytostatic; antitheumatic; antiarthritic; antipsoriatic; antiarteriosclerotic; antidiabetic; antithyroid; excessive neovascularisation; tumour; rheumatoid arthritis; psoriasis; atherosclerosels; diabetes; retrolental fibroplasis; neovascular glaucoma; haemangioma; thyroid hyperplasia; Grave's disease; tissue transplantation; inflammation; oedema; trauma;
                               Gape
                                                                                                                                                                                                                        YO243-1; vascular endothelial cell growth factor; VEGF; antibody;
                               ö
        100.0%; Score 58; DB 2; Length 118; 100.0%; Pred. No. 0.14; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                   Anti-VEGF antibody YO238-3 heavy chain variable domain.
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 14B; 60pp; English
                                                                                                                                  AAB13383 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                 50. .66
/label= CDR-H2
70. .79
/label= CDR-7
                                                                                                                                                                                                                                                                                                                                                            16. .35
/label= CDR-H1
                                                                                                                                                                                                                                                                                                                                                                                                                            99. .112
/label= CDR-H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00218481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US029475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van Bruggen N, Perrara N;
                                                                                                                                                                             21-NOV-2000 (first entry)
Ouery Match
Best Local Similarity 100.
                                                      GYTPTNYGIN 10
                                                                   GYTFTNYGIN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-442646/38.
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                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2000
                                                                                                                                                        AAB13383;
                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; angiogenesis inhibitor; tumour; retinal disorder; intraocular neovascular disorder; Y0192; heavy chain; variable domain.
                                                                                                                                                            Gaрв
hybridoma cells and those with affinity for VEGF are identified by immunoprecipitation or by an in vitro binding assay
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                                                                                                             100.0%; Score 58; DB 3; Length 118; 100.0%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised anti-VEGP Y0192 antibody variable heavy domain.
                                                                                                                                                          0; Indels
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                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  ABP61249 standard; protein; 118 AA.
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/label= CDR-H2
70. .79
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/label= CDR-H1
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/label= CDR-H3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-SEP-2002 (first entry)
                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                        1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                GYTPTNYGIN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-517920/55.
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WELLS J A.
PRESTA L G.
LOWMAN H B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002032315-A1.
                                                                        Sequence 118 AA;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                              ABP61249;
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(WELL/)
(PRES/)
(LOWM/)
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Domain
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Gaps

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Length 118; 0; Indels

100.0%; Score 58; DB 5; 100.0%; Pred. No. 0.14; 0; Mismatches

Conservative

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Query Match
Best Local Similarity
           Sequence 118 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endothelial growth factor) antibodies or a variant of a parent anti-VEGF antibody, which binds human VEGF. The anti-VEGF antibodies are useful for inhibiting VEGF-induced angiogenesis in a mammal (particularly a human), particularly those having a tumour or a retinal disorder e.g. intraocular neovascular disorders. The present sequence is an exemplary heavy chain variable domain of the humanised anti-VEGF antibody of the invention
                                                                                                                                                                                                                                                                                           Cytostatic, ophthalmological; humanised; antibody; anti-VEGF; VEGF; vascular endothelial growth factor; angiogenesis inhibitor; tumour; retinal disorder; intraocular neovascular disorder; Y0238-3; heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-VEGF (vascular endothelial growth factor) antibodies or their variants, useful for inhibiting VEGF-induced angiogenesis in a mammal, particularly for treating tumor or retinal disorders.
                                                                          Gaps
the humanised anti-VEGF antibody of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to humanised anti-VEGF (vascular
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                                               Length 118;
                                                                          0; Indels
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                                              100.0%; Score 58; DB 5;
100.0%; Pred. No. 0.14;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                         ABP61253 standard; protein; 118 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                           26. .35
/label= CDR-H1
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/label= CDR-H2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99. .112
/label= CDR-H3
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/label= CDR-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-00056160
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                                                                                                                                                                                                                                            (first entry)
                                                                          Conservative
                                                                                                   1 GYTFTNYGIN 10
                                                                                                                   GYTFTNYGIN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACA M.
WELLS J A.
PRESTA L G.
LOWMAN H B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-517920/55.
                                             Query Match
Best Local Similarity
Matches 10; Conserv
variable domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHEN Y M.
                       Sequence 118 AA;
                                                                                                                                                                                                                                                                                                                                     variable domain.
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                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                            20-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
Synthetic.
                                                                                                                                                                                                                    ABP61253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LOWM/)
                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                   RESULT 6
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The present invention describes an antibody comprising a variant heavy chain hinge region incapable of inter-heavy chain disulfide linkage. Also described: (1) an antibody lacking inter-heavy chain disulfide linkage. Also described: (1) an inmunoconjugate comprising the antibody or immunoconjugate comprising the antibody or immunoconjugate, and carrier; (4) an article of manufacture comprising the composition in a container; (5) a polymucleotide encoding the antibody or immunoconjugate, or a variant immunoglobulin heavy chain carbibody or immunoconjugate, (6) a polymucleotide encoding the antibody or immunoconjugate; (7) a host cell comprising the recombinant vector; (8) expressing in a host cell and comprising the recombinant at least one inter-heavy chain disulfide linkage; (6) an ecombinant of comprising the recombinant at least one inter-heavy chain disulfide inhapped; (7) a host cell comprising the recombinant at least one inter-heavy chain disulfide inhapped; (10) an approsylated antibody produced by the method; and (10) treating, preventing, disagnosing, delaying or preventing, diagnosing, delaying or preventing a disease in a subject. The antibody has cytostatic and immunosuppressive activities, and can be useful for treating, preventing, diagnosing, diagnosing, delaying or preventing a disease, e.g. tumour, cancer or immunoconjugate and methods are useful for treating, preventing, diagnosing disease, e.g. tumour, cancer or immune disorder. The present sequence represents the anti-VEGF heavy chain from the expression cassette of the present the anti-VEGF heavy chain from the expression cassette of the present the anti-VEGF heavy chain from the expression cassette of the present the anti-VEGF heavy chain from the expression cassette of the present the anti-VEGF heavy chain from the expression cassette of the present the composition of the present the composition of the expression cassette.
                                                                                                                                                                                                                                                                                                                                          Plasmid pxVG11VNERK expression cassette heavy chain protein SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                 antibody; variant heavy chain hinge region; immunoconjugate; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibody comprising a variant heavy chain hinge region incapable of inter-heavy chain disulfide linkage, useful for treating, preventing, diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
expression cassette; plasmid pxVG1IVNERK; anti-VEGF heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 12; 124pp; English.
                                                                                                                                                                                     ADO14132 standard; protein; 479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-2003; 2003WO-US034610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-OCT-2002; 2002US-0422952P.
                                                                                                                                                                                                                                                                                              (first entry)
1 GYTFTNYGIN 10
                           GYTFTNYGIN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reilly D, Yansura DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-390607/36.
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                                                                                                                                                                                                                                                                                              12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modifield framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a subsettution of at least one amino acid position with a different amino acid, where the different amino acid is the method described above has a subsettution of a human subgroup variable domain consensus sequence that has a hypervariable region 1 (HYR1) and/or HYR2 sequence with the most sequence identity with a corresponding HYR1 and/or HYR2 sequence of the variable domain.

The antibody or antigen binding fragment variable domain comparied to an cumodified antibody or antigen-binding fragment. The antibody and antigen binding fragment invention are useful for temnomodulatory activities, and can be used in antibody therapy. The methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragments of the invention can be binding fragments of antigen binding fragments and can be used in antibodies or antigen binding fragments and can be used in antibodies or antigen binding fragments and can be used in antibodies or antigen binding fragments and can be used in antibodies or antigen binding fragments and can be used in antibodies or antigen binding fragments and can be also and composition of the present invention and antigen binding fragments in cell culture. The antibodies or antigen binding fragments and antigen binding fragments and antigen binding fragments and antigen binding fra ö Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell. antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; anglogenic disorder; immunological disorder; anti-VEGF antibody; anti vascular endothelial cell growth factor antibody; heavy chain. Gaps ö 100.0%; Score 58; DB 8; Length 479; 100.0%; Pred. No. 0.56; Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:21, 0; Indels Mismatches Example 7; SEQ ID NO 27; 161pp; English. ADQ90737 standard; protein; 479 AA. ö 23-JAN-2004; 2004WO-US001844. 23-JAN-2003; 2003US-0442484P (first entry) 10; Conservative 1 GYTFTNYGIN 10 58 (GETH) GENENTECH INC WPI; 2004-562149/54. 49 GYTFTNYGIN Local Similarity N-PSDB; ADQ90722 Sequence 479 AA; WO2004065417-A2. Homo sapiens 21-OCT-2004 05-AUG-2004 Simmons L; Synthetic ADQ90737; Query Match Matches RESULT 8 ADQ90737

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The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprises expressing a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the antibody or antigen binding fragment variable domain comprising the antiferent amino acid, where the different amino acid is comprising the addition with a different amino acid, where the different amino acid is cost tion with a different amino acid, where the different amino acid is cost and found at the corresponding FR position of a human subgroup variable domain consensus sequence that has a hypervariable region 1 (HYR1) and/or HYR2 amino acid sequence with the most sequence identity ith a corresponding HYR1 and/or HYR2 sequence of the variable domain.

The antibody or antigen binding fragment variable domain comprises the modified FR that has improved yield in cell culture compared to an entigen antibody or antigen-binding fragment. The antibody and antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing an antibody or antigen binding fragment in high yield in a cell culture, comprises expressing a variable domain with a modified framework region in a host cell.
used to diagnose, treat, inhibit or prevent e.g. tumours and inflammatory, anglogenic and immunological disorders. The present sequence represents the heavy chain of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; antigen binding fragment; cell culture; variable domain; modified framework region; hypervariable region; cytostatic; antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy; tumour; inflammatory disorder; angiogenic disorder; immunological disorder; anti-VEGF antibody; anti vascular endothelial cell growth factor antibody; heavy chain.
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        ö
                                                                                                                                                                   8; Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:11.
                                                                                                                                                                                                        0; Indels
                                                                                                                                                                   100.0%; Score 58; DB 8, 100.0%; Pred. No. 0.56;
                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              ADQ90732 standard; protein; 479 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                         GYTFTNYGIN 58
                                                                                                                                                                                                                                                    1 GYTFTNYGIN 10
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N-PSDB; ADQ90706.
                                                                                       present invention
                                                                                                                             Sequence 479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004065417-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simmons L;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ90732;
                                                                                                                                                                                                                                                                                            49
                                                                                                                                                                                                                                                                                                                                                       RESULT 9
ADQ90732
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variable domain consensus sequence that has a hypervariable region 1

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binding fragment have cytostatic, antiinflammatory, antiangiogenic and immunomodulatory activities, and can be used in antibody therapy. The methods and compositions of the present invention are useful for producing antibodise or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and inflammatory, angiogenic and immunological disorders. The present sequence represents the heavy chain of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for producing an antibody or antigen binding fragment in high yield in a cell culture. The method comprises expressing a variable domain of the antibody or antigen binding fragment comprising a modified framework region (FR) in a host cell, and recovering the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid position with a different amino acid, where the different amino acid is the amino acid is the amino acid tound at the corresponding FR position of a human subgroup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified framework region; hypervariable region; cytostatic; antiinflammatory; antianglogenic; immunomodulatory; antibody therapy; tumour; inflammatory; disorder; angiogenic disorder; immunological disorder; anti-VEGE antibody; anti vascular endothelial cell growth factor antibody; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen binding fragment; cell culture; variable domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYTFINYGIN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYTFTNYGIN
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                                                                                                                                                                                                                                                                                                                                                                  present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004065417-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody;
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11D ADQ90729

21 ADQ90729

XX ADQ9

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(HYR1) and/or HYR2 amino acid sequence with the most sequence identity with a corresponding HYR1 and/or HYR2 sequence of the variable domain.

The antibody or antigen binding fragment variable domain comprises the modified FR that has improved yield in cell culture compared to an unaddified antibody or antigen-binding fragment. The antibody and antigen binding fragment bave cytostatic, antiinflammatory, antianglogenic and immunomodulatory activities, and can be used in antibody therapy. The methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture, in particular for improving the yield of recombinant antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and cultiflammatory, angiogenic and immunological disorders. The present sequence represents the heavy chain of an anti-VEGF (vascular endothelial sequence represents the heavy chain of an anti-VEGF (vascular endothelial cell growth factor) antibody, which is used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified framework region; hypervariable region; cytostatic; antiinflammatory; antiangiogenic; immunomodilatory; antibody therapy; tumour; inflammatory; disorder; angiogenic disorder; immunological disorder; anti-vese antibody; antibody; antibody; anti-vese anti-ves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; antigen binding fragment; cell culture; variable domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 58; DB 8; Length 479; 100.0%; Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-VEGF antibody VNERK heavy chain protein SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GYTFTNYGIN 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 479 AA;
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recovering the antibody or antigen binding fragment variable domain comprising the antibody or antigen binding fragment variable domain comprising the modified framework from the host cell. The modified FR in the method described above has a substitution of at least one amino acid position with a different amino acid, where the different amino acid is the amino acid found at the corresponding FR position of a human subgroup the amino acid found at the corresponding FR position of a human subgroup of the amino acid found at the corresponding FR position of a human subgroup (HVR1) and/or HVR2 sequence with the most sequence identity with a corresponding HVR1 and/or HVR2 sequence of the variable domain.

CHA antibody or antigen binding fragment variable domain.

CHA antibody or antigen binding fragment. The antibody and antigen modified R that has improved yield in cell culture compared to an unmodified antibody or antigen-binding fragment. The antibody and antigen handon fragment and antibody and antigen binding fragment and compositions of the present invention are useful for methods and compositions of the present invention are useful for producing antibodies or antigen binding fragments in cell culture. The antibodies of the invention can be used to diagnose, treat, inhibit or prevent e.g. tumours and composition of mamunological disorders. The present inflammatory, anglogenic and immunological disorders. The present sequence represents the heavy chain of an anti-VBGF (vascular endothelial sequence represents the heavy chain of an anti-VBGF (vascular endothelial sequence represents antibody, which is used in the exemplification of the
comprising a modified framework region (FR) in a host
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           888888888888888888888888888
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Sequence 479 AA;

ô Gape ö 100.0%; Score 58; DB 8; Length 479; 100.0%; Pred. No. 0.56; 0; Indels Mismatches ; Local Similarity 100 hes 10; Conservative Query Match Matches

1 GYTPTNYGIN 10

a Š

RESULT 12

ABR83196 standard; protein; 120 AA. ABR83196; **ABR83196**

(first entry) 15-JAN-2004 Chimeric LL1 antibody heavy chain variable region (cLL1VH)

LL1; anti-CD74 antibody; CD-74; cytostatic; immunosuppressive; immunosuppressive; immunomodulator; cLL1; chimeric.

Chimeric - Mus sp.

WO2003074567-A2.

12-SEP-2003.

03-MAR-2003; 2003WO-GB000890.

01-MAR-2002; 2002US-0360259P.

(IMMU-) IMMUNOMEDICS INC. (MCCA/) MCCALL J D.

Goldenberg DM; , g Hansen H, Leung S,

WPI; 2003-767381/72. N-PSDB; ACP57896 New humanized, human or chimeric anti-CD74 antibody or fragment, useful for diagnosing or treating a CD74 expressing malignancy, an immune dysregulation disease, an autoimmune disease or graft versus host

Claim 13; Fig 2A; 91pp; English.

disease.

The invention relates to a humanized, human or chimeric anti-CD74
antibody or its fragment. The naked anti-CD74 antibody or a naked
antibody fusion protein or fragment, or a therapeutic or diagnostic
conjugate comprising an anti-CD74 antibody is useful for diagnosting
treating a disorder or a disease that is a CD74 expressing malignancy
c (solid tumour, non-Hodgkin's lymphoma, Hodgkin's lymphoma, multiple
myeloma, another B-cell malignancy and a T-cell malignancy), an immune
dysregulation disease, an autoimmune disease, organ graft rejection, and
graft versus host disease. The solid tumour is melanoma, carcinoma and
c arcinoma, stomach carcinoma and melanoma. The B-cell malignancy is of
non-Hodgkin's lymphoma, is arenal carcinoma, intestinal
carcinoma, squessive forms of B-cell lymphomas, chronic lymphomas, aggressive forms of B-cell lymphomas, chronic lymphatic leukemias, acute lymphatic leukemias, and multiple myeloma. The present
sequence represents a chimeric anti-CD74 antibody LL1 (cLL1) heavy chain
veriable region

8X8888888888888888

Sequence 120 AA;

Gaps ö DB 7; Length 120; 0; Indels Score 57; DB 7; Pred. No. 0.21; 1; Mismatches 98.3%; Similarity 90.0 9; Conservative Query Match Best Local S Matches

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8 셤 RESULT 13

ABR83194 ID ABR

ABR83194 standard; protein; 120 AA.

15-JAN-2004 (first entry)

ABR83194;

Murine LL1 antibody heavy chain variable region (LL1VH)

LL1; anti-CD74 antibody; CD-74; cytostatic; immunosuppressive; immunomodulator; mLL1

Mus sp.

WO2003074567-A2.

12-SEP-2003

03-MAR-2003; 2003WO-GB000890.

01-MAR-2002; 2002US-0360259P

(IMMU-) IMMUNOMEDICS INC.

(MCCA/) MCCALL J D.

Goldenberg DM; g 2, Hansen H, Leung S,

2003-767381/72. N-PSDB; ACP57894. New humanized, human or chimeric anti-CD74 antibody or fragment, useful for diagnosing or treating a CD74 expressing malignancy, an immune dysregulation disease, an autoimmune disease or graft versus host disease

Claim 6; Fig 3A; 91pp; English.

The invention relates to a humanized, human or chimeric anti-CD74 antibody or its fragment. The naked anti-CD74 antibody or a naked antibody fusion protein or fragment, or a therapeutic or diagnostic conjugate comprising an anti-CD74 antibody is useful for diagnostic treating a disorder or a disease that is a CD74 expressing malignancy (solid tumour, non-Hodgkin's lymphoma, Hodgkin's lymphoma, multiple myeloma, another B-cell malignancy and a T-cell malignancy), an immune

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dysregulation disease, an autoimmune disease, organ graft rejection, and graft versus host disease. The solid tumour is melanoma, carcinoma and sarcoma. The carcinoma and carcinoma, lung carcinoma, intestinal carcinoma, stomach carcinoma and melanoma. The B-cell malignancy is of non-Hodgkin's lymphoma, Hodgkin's lymphoma, indolent forms of B-cell nymphomas, aggreesive forms of B-cell lymphomas, chronic lymphatic leukemias, and multiple myeloma. The present sequence represents a murine anti-CD74 antibody LL1 heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a humanised, human or chimeric anti-CD74 antibody or its fragment. The naked anti-CD74 antibody or a naked antibody or its fragment. The naked antibody or a naked antibody fusion protein or fragment, or a therapeutic or diagnostic conjugate comprising an anti-CD74 antibody is useful for diagnostic treating a disorder or a disease that is a CD74 expressing malignancy (solid tumour, non-Hodgkin's lymphoma, Hodgkin's lymphoma, multiple myeloma, another B-cell malignancy and a T-cell malignancy), an immune disease, another B-cell malignancy and a T-cell malignancy, an immune disease, organ graft rejection, and garft versus host disease. The solid tumour is melanoma, carcinoma and sarcoma. The carcinoma is a renal carcinoma. The B-cell malignancy is of non-Hodgkin's lymphoma, Hodgkin's lymphoma, Hodgkin's lymphoma, Hodgkin's lymphoma, intestinal lymphomas, chronic lymphatic leukemias, acute lymphatic leukemias, and multiple myeloma. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New humanized, human or chimeric anti-CD74 antibody or fragment, useful
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for diagnosing or treating a CD74 expressing malignancy, an immune dysregulation disease, an autoimmune disease or graft versus host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LL1; anti-CD74 antibody; CD-74; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised LL1 antibody heavy chain variable region (hLL1VH)
                                                                                                                                                                                                                          DB 7; Length 120;
                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                          Score 57; DB 7;
Pred. No. 0.21;
                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR83198 standard; protein; 120 AA.
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                                                                                                                                                                                                                        98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 90...
Best Local Similarity 90...
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                                                                                                                                                                                                                                                                                                    1 GYTFTNYGIN 10
                                                                                                                                                                                                                                                                                                                          26 GYTFTNYGVN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunomodulator; httl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-767381/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MCCA/) MCCALL J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ACF57898.
                                                                                                                                                                                         Sequence 120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hansen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR83198;
                                                                                                                                                         region
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sequence represents a humanised anti-CD74 antibody LL1 (hLL1) heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition useful in treating and/or diagnosing, for example, graft-versus-host disease or CD74-expressing malignancy, comprises immunoconjugate having anti-CD74 binding molecules conjugated to lipids,
                                                                                                                                                                                                                                                                                                            immunosuppressive; cytostatic; immunomodulatory; immunotoxin; radioimmunotherapeutic; immunoconjugate; anti-CD744 antibody; CD74-expressing malignancy; immune dysregulation disease; autoimmune disease; corgan-graft rejection; graft-versus-host disease; solid tumor; non-Hodgkin's lymphoma; Hodgkin's lymphoma; Hodgkin's lymphoma; multiple myeloma; B-cell malignancy; T-cell malignancy; melanoma; carcinoma; sarcoma; glioma; mouse; LL1; heavy chain variable region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Complementarity determining region 2"
                                                              Score 57; DB 7; Length 120;
Pred. No. 0.21;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                       Chimeric LL1 antibody heavy chain variable region segid 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffiths GL, Hansen HJ, Goldenberg DM, Lundberg BB;
                                                                                                                                                                                                            ADU26544 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002US-00314330.
2003US-00350096.
2003US-00377122.
2003US-0478830P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-00590284
2001US-00965796
2002US-0360259P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50. .66
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-2003; 2003US-00706852
                                                                  98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31. .35
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99. .109
/label= CDR3
                                                                                                                                                                                                                                                              27-JAN-2005 (first entry)
                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMU-) IMMUNOMEDICS INC
                                                                                                                     1 GYTFTNYGIN 10
                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-010089/01.
N-PSDB; ADU26543.
                                                                 Query Match
Best Local Similarity
                                          Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004219203-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JAN-2003;
03-MAR-2003;
17-JUN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-2004
                                                                                                                                                                                                                                       ADU26544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                   RESULT 15
ADU26544
                                                                                            Matches
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polymeric carriers, and effectors.

Disclosure; SEQ ID NO 6; 44pp; English.

The invention describes a composition (I) comprising an immunoconjugate which has one or more anti-CD74 binding molecules conjugated to one or more lapids, polymeric carriers, micelles, manoparticles or their combinations, and one or more effectors. Also described are: preparing combinations, and one or more effectors. Also described are: preparing combinations, and one or more effectors. Also described are: preparing combinations, and one or more effectors are expensed and anti-CD744 antibody; and a kit comprising (I). (I) is useful for treating and/or antibody; and a kit comprising (I). (I) is useful for treating and/or cationing a disease or disorder such as a CD74-expressing andigease or disorder such as a CD74-expressing malignancy, immune dysregulation disease. The CD74-expressing malignancy is a lymphoma, multiple mysloma, and comparing and gloma. The CD74-expressing malignancy is a solid tumor, which is chosen from melanoma, carcinoma, serome and gloma. The carcinoma, stone from melanoma, prostate cancer, overian cancer, and melanoma. The CD74 expressing malignancy is a solid tumor, which is chosen from melanoma, prostate cancer, overian cancer, and melanoma. The CD74 expressing malignancy is a B-cell malignancy chosen from melanoma, prostate cancer, overian cancer, and melanoma. The CD74 expressing malignancy is a B-cell malignancy chosen from mile comprises LLI or its fragment. The composition further comprises one or more daruge produced in maint-CD30, anti-CD32, anti-CD33, anti-CD33, anti-CD32, anti-CD30, anti-CD33, anti-CD3

Sequence 120 AA;

0; Gaps 98.3%; Score 57; DB 9; Length 120; 90.0%; Pred. No. 0.21; tive 1; Mismatches 0; Indels Query Match
Best Local Similarity 90.0
Matches 9; Conservative

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26 GYTFINYGVN 35 셤 Search completed: April 25, 2006, 06:15:04 Job time : 55.3962 secs

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